

**FIGURE 1**

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCA**ATG**GCGTCCCCGTCTCGGAGAC  
TGCAGACTAAACCAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTC  
TGGATCACTGGCGTTATCCTTCTTGCAAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATTA  
CTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCCCTTCGTGCTCATTGCTACTGGTACCG  
TCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTTCTGCATGGATGCTA  
AAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTAGG  
ATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGC  
AGTATAACTCTACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCAT  
TGTTGTGGTGTCACCGATTATAGAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATT  
TCCTAAGAGTTGCTGTAAACTTGAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA  
ATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGGAGTCGTTGCAGGA  
ATTTCCCTTTGGAGTTGCTTGCTTCCAAGTATTGGAATCTTTCTCGCCTACTGCCWCTCTCG  
TGCCATAACAAATAACCAGTATGAGATAGTG**TAAC**CCAATGTATCTGTGGGCCTATTCCCTCT  
CTACCTTTAAGGACATTTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG  
ACAACACTACTTACTGATAGACCAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT  
GTAGACCTAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGGCTGAT  
TCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTATCCCATTCTATGTTAGATCG  
TTGAAACCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

**FIGURE 2**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA19902
><subunit 1 of 1, 245 aa, 1 stop, 1 unknown
><MW: -1, pI: 8.36, NX(S/T): 1
MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGVSLNENYFSLLEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLLVFLVELVAAIVGVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDNYYSEKGFPSCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRITNNQYEIV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**Transmembrane domains:**

amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**

amino acids 134-138

**Tyrosine kinase phosphorylation site.**

amino acids 160-168, 160-169

**N-myristoylation site.**

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 69-80, 211-222

**FIGURE 3**

CCCACGCGTCCGGCGCCGTGGCCTCGCGTCCATCTTTGCCGTCTCTCGGACCTGTCACAAA  
 GGAGTCGCGCCGCCGCCGCCGCCCTCCCTCCGGTGGGCCCCGGGAGGTAGAGAAAGTCAGT  
 GCCACAGCCCGACCGCGCTGCTCTGAGCCCTGGGCACGCGGAACGGGAGGGAGTCTGAGGGT  
 TGGGGACGTCTGTGAGGGAGGGGAACAGCCGCTCGAGCCTGGGGCGGGCGGACCGGACTGGG  
 GCCGGGGTAGGCTCTGGAAAGGGCCCGGGAGAGAGGTGGCGTTGGTCAGAACCTGAGAAACA  
 GCCGAGAGGTTTTCCACCGAGGCCCGCGCTTGAGGGATCTGAAGAGGTTCCCTAGAAGAGGGT  
 GTTCCTCTTTCCGGGGTCCCTCACCAGAAGAGGTTCTTGGGGGTGCGCCCTTCTGAGGAGGCT  
 GCGGCTAACAGGGCCCAGAACTGCCATTGGATGTCCAGAATCCCCTGTAGTTGATAATGTTG  
 GGAATAAGCTCTGCAACTTTCTTTGGCATTCAAGTTGTTAAAAACAAATAGGATGCAAATTC  
 TCAACTCCAGGTATGAAAACAGTACTTGGAAAACTGAAAACCTACCTAAATGATCGTCTTTG  
 GTTGGGCCGTGTTCTTAGCGAGCAGAAGCCTTGGCCAGGGTCTGTTGTTGACTCTCGAAGAG  
 CACATAGCCCACTTCTTAGGGACTGGAGGTGCCGCTACTACCATGGGTAATTCCTGTATCTG  
 CCGAGATGACAGTGGAACAGATGACAGTGTGACACCCACAGCAACAGGCCGAGAACAGTG  
 CAGTACCCACTGCTGACACAAGGAGCCAACCCACGGGACCTGTTTCGGCCACCAAGGAGGGGC  
 CGAGGACCTCATGAGCCAAGGAGAAAGAAACAAAATGTGGATGGGCTAGTGTGGACACACT  
 GGCAGTAATACGGACTCTTGTAGATAAGTAAAGTATCTGACTCACGGTCACCTCCAGTGGAAT  
 GAAAAGTGTTCGCCCGGAACCATGACTTTAGGACTCCTTCAGTTCCTTTAGGACATACTCG  
 CCAAGCCTTGTGCTCACAGGGCAAAGGAGAATATTTTAATGCTCCGCTGATGGCAGAGTAAA  
 TGATAAGATTTGATGTTTTGCTTGCTGTCATCTACTTTGTCTGGAAATGTCTAAATGTTTC  
 TGTAGCAGAAAACACGATAAAGCTATGATCTTTATTAGAG

## **FIGURE 4**

MIVFGWAVFLASRSLGQGLLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ  
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKQNV DGLVLDTLAVIRTLVDKO

**Signal peptide:**

amino acids 1-16

**Casein kinase II phosphorylation site.**

amino acids 22-26, 50-54, 113-117

**N-myristoylation site.**

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

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**FIGURE 5**

GGCACGAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAGATTAGCCCATTTGGCC  
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGGTTCCTAACGGACTG  
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCCATCTACTGGTCTTGT  
CAGGTGCCTGGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCTGTCTTTCCGAAGC  
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTTCCCCTTCTACTTCCACATCTC  
CATGGGCTGTGCCTTCATCAACCTCTGCATCTTGGCTTCACAGCATGCTTGGGCTCAGCTCA  
CATTCTGGGAGGCCAGCCAGCTTTACCTGCTGTTCCTGAGCCTTACGCTGGCCACTGTCAAC  
GCCCCTGGCTGGAAACCCCGCACCACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA  
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC  
GAGAGAAGGACCCCAAGTACAGTGTCTCTCGCCAGAATTTCTTCCGCTACCATGGGCTGTCC  
TCTCTTTGCAATCTGGGCTGCGTCCTGAGCAATGGGCTCTGTCTCGCTGGCCTTGCCCTGGA  
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**FIGURE 6**

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<NX(S/T): 0
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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFRRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 86-103, 60-75

**Casein kinase II phosphorylation site.**

amino acids 82-86

**Tyrosine kinase phosphorylation site.**

amino acids 144-151

**N-myristoylation site.**

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 54-65

**G-protein coupled receptors proteins.**

amino acids 44-85

**FIGURE 7**

AATTCAGATTTTAAGCCCATCTGCGAGTGAATTTTCATGAACTAGCAAGAGGACACCATCTT  
 CTGTGATTATACAAGAAAGGAGTGACCTATCACACAGGGGAAAAATGCTCTTTTGGGT  
 GCTAGGCCTCCTAATCCTCTGTGGTTTTCTGTGGACTCGTAAAGGAAAACTAAAGATTGAAG  
 ACATCACTGATAAGTACATTTTTATCACTGGATGTGACTCGGGCTTTGGAAACTTGGCAGCC  
 AGAATTTTGATAAAAAGGATTTTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC  
 AGCTTTAAAGGCAGAAACCTCAGAGAGACTTCGTACTGTGCTTCTGGATGTGACCGACCCAG  
 AGAATGTCAAGAGGACTGCCAGTGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGGT  
 CTGATCAATAATGCTGGTGTTCCCGGCGTCTGGCTCCCAGTACTGAGTGGCTGACACTAGAGGA  
 CTACAGAGAACCTATTGAAGTGAACCTGTTTGGACTCATCAGTGTGACACTAAATATGCTTC  
 CTTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTCGCCTTGCA  
 ATCGTTGGAGGGGGCTATACTCCATCCAAATATGCAGTGAAGGTTTCAATGACAGCTTAAG  
 ACGGGACATGAAAGCTTTTGGTGTGCAGCTCTCATGCATTGAACCAAGGATTGTTCAAAACAA  
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 TAAATCCTATGTGAACATGGACCTCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA  
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 TCTCACATGCCAGCAGCTTTGCAAGACTTTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA  
 TCCCAGGCAGTGTGACTCAGCTAACCACAAATGTCTCCTCCAGGCTATGAAATTGGCCGAT  
 TTCAAGAACACATCTCCTTTTCAACCCCATTCCTTATCTGCTCCAACCTGGACTCATTTAGA  
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 ATTTAGGCTTTGCTGCTTGGTGTGATGTAAGGGAATTTGAAAGACTTGCCCATTCAAAATG  
 ATCTTTACCGTGGCTGCCCATGCTTATGGTCCCAGCATTTACAGTAACTTGTGAATGTT  
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**FIGURE 8**

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><subunit 1 of 1, 319 aa, 1 stop
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LTLEDYREPIEVNLFGLISVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSLRRDMKAFGVHVSIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGE GYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTS LFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 136-152

**N-glycosylation sites.**

amino acids 161-163, 187-190 and 253-256

**Glycosaminoglycan attachment site.**

amino acids 39-42

**N-myristoylation sites.**

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212



CGGGGCTGTTACGCGGCTGCC**CAT**GGCTGCCGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT  
CCTCTCAGTCGGGACTTCTGACGCCGCCGATGGGCGGGGCCCTTGGGCGCTGCCACCACT  
GTAGTCATGTACCCACCGCCGCCGCCGCTCATCGGAGCTTCATCTCGTGACGCTGAG  
CTTTGGCGAGAGCTATGACAAACAGCAAGAGTTGGCGCGCGCTCGTGCTGGAGGAAATGGA  
AGCAACTGTCGAGATTGCAGCGGAATATGATTCTCTTCTCTCTGCTTCTGCTTTCTGTT  
GGACTCTCTCTTACATCAACTTGGCTGACCATTGGAAAGCTCTGGCTTTCAGGCTAGAGGA  
AGAGAGCAAGATGAGGCCAGAAATTTGCTGGGTAAACACAGCAAACTCACCCGCTCTTACAGC  
CTCTTCAGAAGCGGACACCGCTGAGAACTTACCTGAGATTTCGTACAGAACAGACAA  
AGACACATCCAGCGGGGACCACTCACCTGCAGATTAGACCCCCAAGCCAAGACTGAAGGA  
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GAGTGGTTTTGGCTCTCGGTCTCACACTGATCGACGCGCTGGACACCATGTGGATCTTGGGTCT  
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GAGCTCTCCCGCTCTACAGGGGTAGAAGAACTTTCAGGAGCGATGGAGAAGTGCACAGCA  
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GCCTCTTACCCACCTTGGCGTATTACGCTGGGCGCCAGGCGCCAGCTACTATGAGTAC  
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GCTCATGGAGACTTGTACCAGATGAACCGGCAGATGAGACGGGGCTGAGTCCGAGATCG  
TGCACTTCAACTTTTACCCCAGCGGGCGCTCGGAGCTGAGGTTCAACCGCAGCAGACAGG  
CACAACTGCTGCGGCACAGACCGTGGAGAGCTGTTCTACTGTACCGGCTCAGAGGGA  
CCGCAAATACAGGACTGGGCTGGGAGATTCTGCAGAGCTTCAGCCGATTACACAGGGTCC  
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AAGATTGAGAGCTTCTCTCGGGGAGACGCTCAAGATGCTGTTCTGTGCTTCTCCGATGA  
CCCAAACTGCTGACGCTGGACGCTTACTGTTTCAACACCGAAGCCACCTCTGCTATCT  
GGACCCCTGCGC**TAG**GGTGGATGGCTGCTGGGTGGGGGATTCGGGTGGGCGAGCCACTTG  
CTGGGCTGTGGCATTTTCCAGGGCGCTGAGTAGCACCGGCAACGCCAAGTGCCCAAGGCT  
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GGCCGTCAGTCTGTGTGTGATGCGGGTGGGCTGGGCGGCTGGAGCCCTCCGCTGCTTCTCT  
CAGAAGACAGCAATCATGACTCACGATTGGCTGAAGCTGAGCAGGTCTCTGTGGGCGACCA  
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TCTGCGCGGGCTCGTGAAGCTCTAGATGTCCCCAATCCAAAGGCTTGAGGGGCTGCGCTGA  
CTCCAGAGGCTTGAGGCTCGAGGCTGGCTCTGGTGTTTACAAGCTGGACTCAGGGAATCTC  
CTGGCGCCCGCCAGGGGGCTTGAGGGCTGGACGGCAAGCTCGCTAGCTCAGCGGCCCCT  
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**FIGURE 10**

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SKSWRRRSCWRKWKQLSRLQRNMILFLAFLFCGLLFYINLADHWKALAFRLLEEQKMRPE
IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTEQEEAT
KRQEAPVDPRPEGDPQRTVISWRGAVIEPEQGTELPSSRAEVP TKPPLPPARTQGTVPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVRSRSEWFGGLGLTLIDALDTMWILGLRKEFEEA
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PYSDVNIGTGVAHPRWTS DSTVAEVT SIQLEFRELSRLTGDKKFQEA VEKV TQHIHGLSGK
KDGLVPMFINTHSGLFTHLGVFTLGARADSYEYLLKQW IQGGKQETQLLEDYVEAIEGVRT
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MNRQMETGLSPEIIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFRTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFLLFSDDPNLLSLD
AYVFNTAEHPLPIWTPA
```

**Important features of the protein:**

**Transmembrane domain:**

amino acids 21-40 and 84-105 (type II)

**FIGURE 11**

GGC GCCCGCTAGGCCCGGGAGGCCGGGCCGGGCTGCGAGCGCCTGCCCCATGCGCCGC  
 CGCCTCTCCGCACG**ATG**TTCCCCTCGCGGAGGAAAGCGGCGCAGCTGCCCTGGGAGGACGGC  
 AGGTCGGGTTGCTCTCCGGCGGCCTCCCTCGGAAGTGTTCCGTCTTCCACCTGTTTCGTGGC  
 CTGCTCTCGCTGGGCTTCTTCTCCCTACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG  
 CCCGGGCAGTCAGGGGACAAGGGCAGGAGACCTCGGGCCCTCCCGTGCTGCCCCCAGAG  
 CCGCCCCCTGAGCACTGGGAAGAAGACGCATCCTGGGGCCCCACCGCTTGGCAGTGCTGGT  
 GCCCTTCCGGAACGCTTCGAGGAGCTCCTGGTCTTCGTGCCCCACATGCGCCGCTTCTCTGA  
 GCAGGAAGAAGATCCGGCACCACATCTACGTGCTCAACCAAGTGGACCACTTCAGGTTCAAC  
 CGGGCAGCGCTCATCAACGTGGGCTTCCTGGAGAGCAGCAACAGCACGGACTACATTGCCAT  
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTTCCTGAGGCTGGGC  
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 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGGATGTCCAACCGCTTCTGGGG  
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 AGCTACGCAATTGCAGCCACCCGGCCGCAAGGCAGGCTTGGGCTGGGCCAGGACACGTGGG  
 GTGCCTGGGACGCTGCTTGCCATGCACAGTGATCAGAGAGAGGCTGGGGTGTGCTCTGTCCG  
 GGACCCCCCTGCCTTCTGTCTACCCCTACTCTGACCTCCTTCACGTGCCAGGCCTGTGGG  
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**FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56531  
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RHHIYVLNQVDHFRFNRAALINVGFLSSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA  
SPELHPLYHYKTYVGGILLLSKQHYRLCNGMSNRFWGWGREDDFYYRIKAGLQLFRPSGI  
TTGYKTFRHLHDPAWRKRDQKRIAQAQKQEQFKVDREGGLNTVKYHVASRTALSVGGAPCTVL  
NIMLDCDKTATPWCTFS

**Signal peptide:**

amino acids 1-42

**Transmembrane domain:**

amino acids 29-49 (type II)

**N-glycosylation site.**

amino acids 154-158

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 27-31

**Tyrosine kinase phosphorylation site.**

amino acids 226-233

**N-myristoylation site.**

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

**FIGURE 13**

CAATGTTTGCCTATCCACCTCCCCCAAGCCCCTTTACCT**ATG**CTGCTGCTAACGCTGCTGCT  
GCTGCTGCTGCTGCTTAAAGGCTCATGCTTGGAGTGGGGACTGGTCGGTGCCAGAAAGTCT  
CTTCTGCCACTGACGCCCCCATCAGGGATTGGGCCTTCTTTCCCCCTTCCTTTCTGTGTCTC  
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCAGCCCCGTGGGGAAGGGGAGAAAGT  
GGGGGATGGCT**TAA**GAAAGCTGGGAGATAGGGAACAGAAGAGGGTAGTGGGTGGGCTAGGGG  
GCTGCCTTATTTAAAGTGTTGTTTATGATTCCTATACTAATTTATACAAAGATATTAAGGC  
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**FIGURE 14**

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PRGEGEKVGDG

```

**Important features:****Signal peptide:**

amino acids 1-15

**Growth factor and cytokines receptors family:**

amino acids 3-18

**FIGURE 15**

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG  
 GAGCATGTCCGCGCCGGGGAAGGCCCGTCTCCGCGCCGCATAAAGGCTCCGGTCCGCGCTGG  
 GCGCGCGCCGCGCTCTTGCCCGCCGGGCTCCGGGCGGCCGTAGGCCAGTGCGCCGCCG  
 CTCGCCCCGAGGCCCGCGCCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGGCCGCGCGCA  
 GCCGCGCGTGTTGCTGCCGCTCTCGCTGTTAGCGCTGCTCGCGCTGCTGGGAGGCCGCGCGC  
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 GACAAACAATCGAATAGGATGTCTGAATGCAGACATATTTCCGAGGACTCACCAATCTGGTTC  
 GGCTAAACCTTTCCGGGAATTGTTTTCTTCATTATCTCAAGGAACCTTTTGATTATCTTGCG  
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 TCCTTTCCAGTGCATGGCTTCATATATTGATCAGGACATGCAAGTGTGTGGTATCAGGATG  
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 TGCTCCTTAGTTCGAAGTGCCTAACCACTTTCTAATATTCCAGCTGGATCTACTGGAATTG  
 GGGCTGTGATGTCCAGACCAACGTGGGAATAATACGAGGACTGTGGATATTGTGGTATTAG  
 AGAGTTCTGCACGATATGTCTCCAGAGAGGGTGGTAAACAACAAAGGTGACTTCAGATGG  
 CCCAGAACATTGGCAGGCATTAAGTGCATATCTGCAGTGTACGCCGAACACCCATGGCAGTGG  
 GATATATCCCGGAAACCCACAGGATGAGAGAAAAGCTTGGCGCAGATGTGATAGAGGTGGCT  
 TTTGGGCAGATGATGATTATCTCGCTGTCAGTATGCAATGATGTCACTAGAGTCTCTTAT  
 ATGTTTAAATCAGATGCCCTCAATCTTACCAATGCCGTGGCAACAGCTCGACAGTTACTGGC  
 TTACACTGTGGAAGCAGCCAACTTTTCTGACAAAAATGGATGTTATATTGTTGGCAGAAATGA  
 TTGAAAAATTTGGAAGATTTACCAAGGAGGAAAAATCAAAAGAGCTAGGTGACGTGATGGTT  
 GACATTGCAAGTAACATCATGTTGGCTGATGAACGTGTCTGTGGCTGGCGCAGAGGGAAGC  
 TAAAGCCTGCAGTAGGATGTGTCAGTGTCTTACGCGCATTGCTACCTACCGGCTAGCCGGTG  
 GAGCTCACGTTTTATTCACATATTACCCCAATTATGCTCTGGAAGCTTATGTCATCAAGTCT  
 ACTGGCTTCACGGGATGACCTGTACCGTGTTCAGAAAGTGGCAGCCTCTGATCTCAGAGG  
 ACTTTCCGATGTGGGAGCGGGATCCAGAGGAACTCGGATAAGCAGCTGAGCTTTTAAAGT  
 GCAATGTTTCAAATACATTTTTCGAGTCTGGCACTAAAGGTATGTTACATTCTGCAATCATTT  
 AAGACTATTTACAGT**TAA**ATTAGAATGCTCCAAATGTTCTGCTTCGCAAAATAACCTTATTA  
 AAAGATTTTTTTTGCAGGAAGATAGGTATTATTGCTTTTGGCTTTTAAAGAACTA  
 ACCAGGAAGAATGCATTACGACTTTCAAGGGCCCTAGGCAATTTTTGCTTTTGATTCCCTTT  
 CTTTCATAAAAATATCAGAAATTACATTTTATAACTGCAGTGGTATAAATGCAAAATATACT  
 ATGTTACATGTGAAAAAATTTTTTGAATTTAAAGTTTATTTATTTGTTTTTTTGGCTCCCT  
 GATTTTAAAGACATAAGATGTTTTATGGGCCCTTAAAGTATCATGAGCCTTTGGCACTGC  
 GCTGCCAAGCCTAGTGGAGAGTCAACCTGAGACCAGGTGTTTAAATCAAGCAAGCTGTAT  
 ATCAAAATTTTTTGGCAGAAAAACAAATATGTCATATATCTTTTTTAAAAAAGTATTTCAT  
 TTGAAGCAAGCAAAATGAAGCATTTTACTGATTTTTTAAATTTGGTGCTTTAGATATATTT  
 GACTACCTGTATTTGAAGCAAAATAGAGGAGGCACAACCTCCAGCACCTAATGAACACATTT  
 TTTTTACATTAGCTTTCTGTGGGCATGTGAATTGTATTCTCTGGCGTTTAAATCTCACAG  
 TACTTTATTTCTGTCTTGTCCCTCAATAATATCAAAACAATATCCAGTCATTTTAAATGGC  
 TGCATAAATCACTGACCAACAGGTGTTAGGTGTCTGGTTAGTGTAGCACTCAATAAATA  
 TTGAATGAATGAACAAAAA

**FIGURE 16**

MEPPGRRRRGRAQPPLLLPLSLLALLLGGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK  
 VVCSSELELAQVLPDTPNRTVTILISNNKISELKNGSFSGLSLLERLDLRNNLISSIDPGA  
 FWGLSSLKRDLTNNRIGCLNADIFRGLTNLVRNLNSGNLFSSLSQGTFDYLA SLRSLEFQT  
 EYLLCDCNIIWMHRWVKEKNITVRDTRCVYPKSLQAQPVTVGVKQELTCDPPELPSFYMT  
 SHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGI FVEKNMIHNCSLIASALT  
 ISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGD FRWPRTL  
 GITYLQCTRNTHGSGIYPGNPQDERKAWRRCDRGGFWADDDYSRCQYANDVTRVLYMFNQ  
 MPLNL TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGFRFTKEEKSKELGDMV  
 MVDIASNIMLA DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAY  
 VIKSTGFTGMTCT VFQKVAASDRTGLSDYGRDPEGNLDKQLSFKCNVSNTFSSLALKV  
 CYILQSFKTIYS

**Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 13-40 (type II)

**N-glycosylation site.**

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336,  
 433-437, 453-457, 592-596

**N-myristoylation site.**

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57,  
 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326,  
 384-390, 403-409, 554-560



**FIGURE 17**

GC GTGGGG **ATG** CTAGGAGCTCGAAGGTGGTGTGGGCCTCTCGGTGCTGCTGACGGCGGCC  
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT  
CAGAGACATTGAGAGGCCAAATTCGGAAAAAAGAAAACATTCGTCTTTTGGGAGAACAGATTA  
TTTTGACTGAGCAACTTGAAGCAGAAAGAGAGAAGATGTTATTGGCAAAGGATCTCAAAA  
TCAT**TGA**CTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTTGTGTGTGTGTGTGAT  
GGAGAGTAGCTTAGTAGTATCTTCATCTTTTTTTTTTGGTCACTGTCCTTTTAACTTGATCA  
AATAAAGGACAGTGGGTCATATAAGTTACTGCTTTCAGGGTCCCTTATATCTGAATAAAGGA  
GTGTGGGCAGACACTTTTTGGAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG  
TCACTGTCCAGTGCTTAGGGTTGTTACTGAGAAGCACTGCCGAGCTTGTGAGAAGGAAGGGA  
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAACA  
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGAGGGGAGAGACGCTCCTGATCGTCGAATCC

1000  
900  
800  
700  
600  
500  
400  
300  
200  
100  
0

**FIGURE 18**

MSRSSKVVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**Signal peptide:**

amino acids 1-21

MSRSSKVVVLGLSVLLTAATVAGVHVKKQQWDQQRLRDGVIRDIERQIRKKENIRLLGEQIILT  
EQLEAEREKMLLAKGSQKS

**FIGURE 19**

CTGTCGTCTTTGCTTCAGCCGACGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTTT  
 CAAGTGTGGCTTAATCCGCTCTCCACCACCAGATCTTTCTCGTGGATTCTCTGCTAAGACC  
 GCTGCCATGCCAGTGACGGTAACCCGACCACCATCACAAACCACGACGTCATCTTCGGG  
 CCTGGGGTCCCCCATGATCGTGGGGTCCCCTCGGGCCCTGACACAGCCCTGGGTCTCCTTCGC  
 CTGCTGCAGTGGTGTCTACCTGCGTGGCCTTCTCGCTGGTGGCTAGCGTGGGCGCCTGGAC  
 GGGGTCCATGGGCAACTGGTCCATGTTACCTGGTGTCTTGCTTCTCGTGACCCTGATCA  
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTGGCGCAACTTCCCC  
 ATCACCTTCGCCTGCTATGCGGCCCTCTTCTGCCTCTCGGCCTCCATCATCTACCCACCAC  
 CTATGTCCAGTTCCTGTCCCACGGCCGTTTCGCGGGACCACGCCATCGCCGCCACCTTCTTCT  
 CCTGCATCGCGTGTGTGGCTTACGCCACCGAAGTGGCTGGACCCGGGCCCGGCCGGCGAG  
 ATCACTGGCTATATGGCCACCGTACCCGGGCTGCTGAAGGTGCTGGAGACCTTCGTTCGCTG  
 CATCATCTTCGCGTTTCATCAGCGACCCCAACCTGTACCAGCACCAGCCGGCCCTGGAGTGGT  
 GCGTGGCGGTGTACGCCATCTGCTTCATCTTACGCGCCATCGCCATCTGCTGAACCTGGGG  
 GAGTGACCAACGTCGTACCCATCCCCTTCCCACTTCCTGTGCGGGCTGGCCTTGCTGTG  
 TGTCTCCTCTATGCCACCGCCCTTGTTCCTGCGCCCTCTACCAGTTCGATGAGAAGTATG  
 GCGGCCAGCCTCGGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCTACTACGTGTGT  
 GCCTGGGACCGCGACTGGCTGTGGCCATCCTGACGGCCATCAACCTACTGGCGTATGTGGC  
 TGACCTGGTGACCTCTGCCCACCTGGTTTTTGTCAAGGTCTTAAGACTCTCCCAAGAGGCTCC  
 CGTTCCTCTCCAACCTCTTTGTTCTTCTTGCCTGCTCCCTCCCTCCACCTTTTCTTCTTCC  
 TCCGCTTTCTCTGTTTTCTTCTTCTGCTCTCCCTCCCTCCACCTTTTCTTCTTCTTCC  
 CAATTCTTGACCTCTAACCAGTTCCTGGATGCATCTTCTCCTTCCCTTTCTCTTGTGCTGT  
 TTCCTTCCTGTGTTGTTTTGTTGCCACATCCTGTTTTACCCCTGAGCTGTTTCTCTTTTT  
 CTTTTCTTTCTTTTTTTTTTTTTTTTTTTAAGACGGATTCTCACTCTGTGGCCAGGCTGGAG  
 TGCAGTGGTGCGATCTCAGCTCACTGCAACCCCGCCTCCTGGGTTCAAGCGATTCTCCTCC  
 CCCAGCCTCCCAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGACCCAGCCTGTTTCTCTTT  
 TTCCACTCTTCTTTTTCTCATCTCTTTCTGGGTTCCTGTGCGCTTCTTATCTGCCTGT  
 TTTGCAAGCACCTTCTCCTGTGTCTTGGGAGCCCTGAGACTTCTTCTCTCCTTGCCCTCA  
 CCCACCTCCAAAGGTGCTGAGCTCACATCCACACCCCTTGACGCGTCCATGCCACAGCCCC  
 CCAAGGGGCCCCATTGCCAAAGCATGCCTGCCACCCCTCGCTGTGCGCTTAGTCAGTGTGTAC  
 GTGTGTGTGTGTGTGTTGGGGGGTGGGGGGTGGGTAGCTGGGGATTGGGGCCTCTTTCT  
 CCCAGTGGAGGAAGGTGTGCAGTGTACTTCCCCTTTAAATTAAAAAACATATATATATATAT  
 ATTTGGAGGTGAGTAATTTCCAATGGGCGGGAGGCATTAAGCACGACCCCTGGGTCCCTAGG  
 CCCCCTGGCACTCAGCCTTGCCAGAGATTGGCTCCAGAATTTTGGCAGGCTTACAGAACAC  
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGGCTGGATGCCTTTCATCCCACTATTCT  
 CTGTGGTATGAAAAAG

**FIGURE 20**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
<MW: 35274, pI: 8.57, NX(S/T): 1
MPVTVTTRTTITTTTSSSGLGSPMIVGSPRALTQPLGLRLQLVSTCVAFSLVASVGAWTG
SMGNWSMFTWCFCFSVTLLIILIVELCGLQARFPLSWRNFPIITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIAATFFSCIACVAYATEVAWTRARPEITGYMATVPGLLKVLETFFVACI
IFAFISDPNLYQHQPALWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSFLSGLALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRLAVAILTAINLLAYVAD
LVHSAHLVFVKV

```

**Important features:****Transmembrane domains:**

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,  
205-226, 235-255 and 294-312

**N-glycosylation site.**

amino acids 66-69

**Glycosaminoglycan attachment site.**

amino acids 18-21



**FIGURE 22**

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPFSPKVMHMDPNYCHPSTSLHLCS  
 LAWSFTRLLHPPLSPGISQVVVDHVTKTAMAAQGRVAHLIEWKWSKPSDSPAALESASFSSY  
 SDLSEGEQEAREFAAGVAEQFAIAEAKLRAWSSVDGEDSTDDSYDEDFAGGMDTDMAGQLPLG  
 PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVSPDTLCSSLCSLEDGLLGSFARLASQLLGDE  
 LLLAKLPPSRESAFRSLGPLEAQDSLNSPLTESCLSPAEEEPAPCKDCQPLCPPLTGSWER  
 QRQASDLASSGVVSLDEDEAEPEEQ

**Signal peptide:**

amino acids 1-15

**Casein kinase II phosphorylation site.**

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,  
 285-289, 324-328

**Tyrosine kinase phosphorylation site.**

amino acids 44-52

**N-myristoylation site.**

amino acids 17-23, 26-32, 173-179

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 11-22

**FIGURE 23**

GGTTCCTGGGCGCTCTGTTACACAAGCAAGATACAGCCAGCCCCACCTAAATTTGTTTCCCT  
GGCACCCCTCTGCTCAGTGCACATTGTACACCTAACCCTATCTGTTTCTCTAATGCACGA  
CAGATTCCCTTCAGACAGGACAACCTGTGATATTTTCAGTTCCTGATTGTAATACCTCCTAAG  
CCTGAAGCTTCTGTTACTAGCCATTGTGAGCTTCAGTTTCTTCATCTGCAAAATGGGCATAA  
TACAATCTATTCTTGGCACAATCAAGGGATTGTTATTCTTTAAAAAAAACCAATACCAAAG  
AAGCCTACAA**ATG**CTTGGCCTTAGCCAAAATTCTGTTGATTTCAACGTTGTTTTATTCACTTCT  
ATCGGGGAGCCATGAAAAAGAAAATCAAGACATAAACACAACACAGAACATTGCAGAAGTTT  
TTAAACAATGAAAAATAAACCTATTTCTTTGGAAAGTGAAGCAAACCTAAACTCAGATAAA  
GAAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCGCCCTCCTTTGAATCTACCCAACAA  
CAGCCACGGAATAACAGATTTCTCCAGTAACCTCATCAGCAGAGCATTCTTTGGGCAGTCTAA  
AACCCACATCTACCATTCCACAAGCCCTCCCTTGATCCATAGCTTGTTTCTAAAGTGCCCT  
TGGAATGCACCTATAGCAGATGAAGATCTTTTGCCCATCTCAGCACATCCCAATGCTACACC  
TGCTCTGTCTTCAGAAAACCTTCACTTGGTCTTTGGTCAATGACACCGTAAAACTCCTGATA  
ACAGTTCCATTACAGTTAGCATCCTCTCTTCAGAACCAACTTCTCCATCTGTGACCCCCCTTG  
ATAGTGGAACCAAGTGGATGGCTTACCACAAACAGTGATAGCTTCACTGGGTTTACCCTTA  
TCAAGAAAAAACCACTCTACAGCCTACCTTAAATTCACCAATAATTCAAAACCTCTTTCCAA  
ATACGTCAGATCCCCAAAAAGAAAATAGAAATACAGGAATAGTATTGCGGGCCATTTTAGGT  
GCTATTCTGGGTGTCTCATTGCTTACTCTTGTGGGCTACTTGTTGTGGAAGGAAAAC  
GGATTCAATTTCCCATCGCGACTTTATGACGACAGAAATGAACAGTTCTGCGATTAGACA  
ATGCACCGGAACCTTATGATGTGAGTTTGGGAATTCAGCTACTACAATCCAACCTTTGAAT  
GATTTCAGCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCCCTATGGATGACATACC  
TCCACTTCGTACTTCTGTAA**TAGA**ACTAACAGCAAAAAGGCGTTAAACAGCAAGTGTCATCTA  
CATCTAGCCTTTTGACAAATTCATCTTTCAAAGGTTACACAAAATTACTGTCACGTGGAT  
TTTGTCAAGGAGAATCATAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT  
CCAAAGGTTTTCTTCTTACAATTTTTGGCCATCCTGAGGCATTTACTAAGTAGCCTTAATT  
TGTATTTTAGTAGTATTTCTTAGTAGAAAATATTTGTGGAATCAGATAAAACTAAAAGATT  
TCACCATACAGCCCTGCCTCATAACTAAATAATAAAAATTTATCCACCAAAAAATCTAAA  
ACAATGAAGATGACTCTTTACTGCTCTGCCTGAAGCCCTAGTACCATAATTCAAGATTGCAT  
TTTCTTAAATGAAAATTGAAAGGGTGCTTTTTAAAGAAAATTTGACTTAAAGCTAAAAAGAG  
GACATAGCCCAGAGTTTCTGTTATTGGGAAATTGAGGCAATAGAAATGACAGACCTGTATTC  
TAGTACGTTATAATTTCTAGATCAGCACACACATGATCAGCCCACTGAGTTATGAAGCTGA  
CAATGACTGCATTCAACGGGGCCATGGCAGGAAGCTGACCCATCCCAAGGAAAGTAATAGCT  
TCTTTAAAGTCTTCAAAGGTTTTGGGAATTTAACTTGCTTAATATATCTTAGGCTTCAA  
TTATTTGGGTGCCTTAAAACTCAATGAGAATCATGGT

**FIGURE 24**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSLLSGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPLIHSFVSKVPWNA
PIADEDLLPISAHPNATPALSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTNSDSFTGFTPQEKTTLQPTLKFTNNSKLPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSESHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNDSA
MPSEENARDGIPMDDIPPLRTSV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domain:**

amino acids 235-262

**N-glycosylation site.**

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,  
163-167, 218-222, 225-229, 298-302, 307-311



**FIGURE 25**

AACAGGATCTCCTCTTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTTACCGCGC  
 AGCCCGAAGATTCACT**ATG**GTGAAAAATCGCCTTCAATACCCCTACCGCGCTGCAAAAGGAGG  
 AGGCGCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC  
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT  
 CTTAGGCCTTTCATTCATCTTGGCAGGACTTATTGTTGGTGGAGCCTGCATTTACAAGTACT  
 TCATGCCCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTTTTGATTCTGAGGATCCTGCA  
 AATTCCCTTCGTGGAGGAGAGCCTAACTTCCTGCCTGTGACTGAGGAGGCTGCATTCGTGA  
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTTCTCTGATAGTGACCTGAG  
 CAATTATTTCATGACTTTGAAAAGGGAATGACTGCTTACCTGGACTTGTGTGGGGAACTGC  
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAATCTGGTAGAGCTCTTTGG  
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTTATGTGGTTCGAGAAGACCTAGTTGCTG  
 TGGAGGAAATTCGTGATGTTAGTAACCTTGGCATCTTTATTTACCAACTTTGCAATAACAGA  
 AAGTCCTTCCGCCCTTCGTCGAGAGACCTCTTGCTGGGTTTCAACAAACGTGCCATTGATAA  
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTTATTGTTGAGACCAAGACTCTGTCAAGAG**T**  
**AA**GAGGCAACAGATAGAGTGTCTTGGTAATAAGAAGTCAGAGATTTACAATATGACTTTAA  
 CATTAAAGGTTTATGGGATACTCAAGATATTTACTCATGCACTTTACTCTATTGCTTATGCTTT  
 AAAAAAAGGAAAAAAAAAAAAAACTACTAACCCTGCAAGCTCTTGTCAAATTTTAGTTTAAT  
 TGGCATTGCTTGTTTTTTGAAACTGAAATTACATGAGTTTCATTTTTTCTTTGCATTTATAG  
 GGTTTAGATTTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAAATTCATCC  
 GTTGTTTTTTTTGTGTTTGTGTTTTTCTTTTCTTTAAGTAAGCTCTTTATTCATCTTATG  
 GTGGAGCAATTTTAAATTTGAAATATTTTAAATTGTTTTTGAACCTTTTGTGTAATAATA  
 TCAGATCTCAACATTGTTGGTTTCTTTTGTGTTTTTCATTTTGTACAACTTCTTGAATTTAGA  
 AATTACATCTTTGAGTTCTGTTAGGTGCTCTGTAATTAACTGACTTATATGTGAACAATT  
 TTCATGAGACAGTCATTTTTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG  
 AATGCACAAAATTTGTGTAGGTGCTGAATGCTGTAAGGAGTTTAGGTTGTATGAATTCACAA  
 CCTATAATAAATTTTACTCTATACAAAAA

**FIGURE 26**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
<subunit 1 of 1, 263 aa, 1 stop
<MW: 29741, pI: 5.74, NX(S/T): 1
MVKIAFNTPTAVQKEEARQDVEALLSRTVRTQILTGKELRVATQEKEGSSGRCLTLLGLSF
ILAGLIVGGACIYKYFMPKSTIYRGEMCFFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLGNCYLMPLNTSIVMPKKNLVELFGKLAGS
RYLPQTYVVREDLVAVEEIRDVSNLGIFYQLCNNRKSFRLRRRDLLGFNKRAIDCKWKIR
HFPNEFIVETKICQE

```

**Type II transmembrane domain:**

amino acids 53-75

**N-glycosylation site.**

amino acids 166-170

**Casein kinase II phosphorylation site.**

amino acids 35-39, 132-136, 134-138

**N-myristoylation site.**

amino acids 66-72, 103-109

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 63-74

**FIGURE 27**

GGAGGAGGGAGGGCGGGCAGGCGCCAGCCAGAGCAGCCCCGGGCACCCAGCAGCGACTCTCT  
CTTCCAGCCAGGTGCCCCCACTCTCGCTCCATTGGCGGGAGCACCAGTCTGTACGCC  
AAGGAACTGGTCTTGGGGGCACC**ATG**GTTTCGGCGGCAGCCCCAGCCTCTCATCTCTCTG  
TTGCTGCTGCTGGGGTCTGTGCCTGCTACCGACGCCCGCTCTGTGCCCTGAAGGCCACGTT  
CCTGGAGGATGTGGCGGGTAGTGGGAGGCCGAGGGCTCGTCGGCTCTCTCCCGAGCCTCC  
CGCCACCTGGACCCCGGCCCTCAGCCCACTCGATGGGGCCCCAGCCACAAACCTGGGG  
GGCCCATACCCCCACCAACTTCCTGGATGGGATAGTGGACTTCTTCCGCCAGTACGTGAT  
GCTGATTGCTGTGGTGGGCTCCCTGGCCTTTCTGCTGATGTTTCATCGTCTGTGCCGCGGTCA  
TCACCCGGCAGAAGCAGAAGGCCTCGGCCTATTACCCATCGTCTCTCCCAAGAAGAAGTAC  
GTGGACCAGAGTGACCGGGCCGGGGGCCCGGGGCCCTTCAGTGAGGTCCCCGACAGAGCCCC  
CGACAGCAGGCCCCGAGGAAGCCCTGGATTCTCCCGGCAGCTCCAGGCCGACATCTTGGCCG  
CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGGCGGTGGGGACGGAGCCAGGATG  
GTGGAGGGCAGGGGCGCAGAGGAAGAGGAGAAGGGCAGCCAGGAGGGGACCAGGAAGTCCA  
GGGACATGGGGTCCCAGTGAGACACCAGAGGCGCAGGAGGAGCCGTGCTCAGGGGTCCCTG  
AGGGGGCTGTGGTGGCCGGTGAGGGCCAAGGGGAGCTGGAAGGGTCTCTCTTGTAGCCCAAG  
GAAGCCAGGGACCAGTGGGTCCCCCGAAAGCCCTGTGCTTGCAGCAGTGTCCACCCAG  
TGTC**TAA**CAGTCTCTCCGGGTGCCAGCCCTGACTGTGCGGCCCCCAAGTGGTCACCTCCCC  
GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTTGGCCTCCCTGTGG  
TGCCAATCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCGGTGCCCGGA  
GGAATCTTACCAAGTGCCATCATCTTCACCTCAGCAGCCCCAAAGGGCTACATCTTACAGC  
ACAGTCTCCCTGACAAAGTGAGGGAGGGCAGTGTCCCTGTGACAGCCAGGATAAAACATCC  
CCCAAAGTGTGGGATTACAGGCGTGAGCCACCGTGCCCGGCCCAAACACTTTTAAAAACA  
GCTACAGGGTAAATCTGACAGCACCACCTCTGGAAAATACTGCTCTTAATTTTCTGAAGG  
TGGCCCCCTGTTTCTAGTTGGTCCAGGATTAGGGATGTGGGGTATAGGGCATTAAATCCTC  
TCAAGCGCTCTCCAAGCACCCTCGGCCTGGGGGTGAGTTTCTATCCCGCTACTGTGCTGG  
GATCAGGTTGAATGAATGGAACCTTCTCTGTCTGGCCTCCAAAGCAGCCTAGAAGCTGAGGG  
GCTGTGTTTGAAGGGACCTCCACCCTGGGGAAGTCCGAGGGGCTGGGGAAGGGTTTCTGACG  
CCAGCCTGGAGCAGGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGCTCTGGCAGCCTG  
TGTCCACAATATTCTGTCAGTCCCTGCAGGGAGCCCTGGGCTCCGTCTCTGCTTTAGGGAGGCT  
CTGGCAGGAGGTCCCTCTCCCCCATCCCTCCATCTGGGGCTCCCCAACCTCTGCACAGCTCT  
CCAGGTGCTGAGATATAATGCACCAGCACAAATAAACCTTTTATCCGGCTGAAAAAAAAAAAA  
AAA

**FIGURE 28**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAPSLILLILLLLGSPATDARSVPLKATFLEDVAGSGEAGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFFRQYVMLIAVVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPPKKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEKGSQEGDQEVQGHGVPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLAQEAQGPVGPPEPCACSSVHPSV
```

**Signal peptide:**

amino acids 1-25

**Transmembrane domain:**

amino acids 94-118

**N-myristoylation site.**amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,  
211-217, 238-244, 242-248

[illegible][illegible]

**FIGURE 30**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
MKFQGPLACLLALLCLSGEAGPLQSGEESTGTNIGEALGHGLGDALSEGVGKAIGKEAGGA
AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGGHIFGSGQGLGGQGQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAWPWGQGGNGGPPNFGTNTQCAVAQPGYGSVRASNQNEGCTNPPPSGSGGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSSGSSSSGSSSSGSSSSGSSSSGSSSGNSGGSRGDSGSESSW
GSSTGSSSGNHGSGGGNGHKPGCEKPGNEARGSGESGIQGFRRGQVSSNMREISKEGNRLL
GGSGDNYRGQGSWSWGGGDAVGGVNTVNSETSPGMFNFDTFWKNFKSKLGFINWDINKDQ
RSSRIP
```

**Signal peptide:**

amino acids 1-21

**N-glycosylation site.**

amino acids 265-269

**Glycosaminoglycan attachment site.**

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

**Casein kinase II phosphorylation site.**

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

**N-myristoylation site.**

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70,  
 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158,  
 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205,  
 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252,  
 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281,  
 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298,  
 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328,  
 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387,  
 383-389, 387-393, 389-395, 395-401

**Cell attachment sequence.**

amino acids 301-304

**FIGURE 31**

GACCGGTCCCTCCGGTCTCGGATGTGCGGACTCTGCTGCAGCGAGGGTGCAGGCCCGCGGGCGGTGCTCACCG  
 TGCCTTGGCTGGTGGAGTTTCTCTCCTTTGCTGACCATTTGTTCCCTTGTCTGGAATATTACCGGGACATCTTCA  
 CTCTCCTGCTGCGCTGCACCGGAGCTTGGTGTGTGCGAGGAGTGGAGGGAATATGTTGTTTCTGAACAAGC  
 TGCTGCTACTTGTGTCCTGGGCTGGCTTTTCCAGATTCCACAGTCCCTGAGGACATGTTCTTTCTGGAAGAGG  
 GTCCCTCATATGCTTGGCTTGGATGTGATACAGTACGCCACAGAGCATGGCTTGGACAAATGCGCCTGTGGTGGACGAGC  
 AGCTGCTCTACACCTGCTGCCCTACATCGGAGAGCTCCGGAACATGCTCGCTTCTGGTGGTGTGAGGACAGTAGT  
 GACGGAGTGGGGGCTTCATGAGGAAATCACCCACACTACCACAGCTGGGAGGCCAGCCTTCCACAGCCA  
 GCCAGGGGTGCGAGCACAGCTCGCCAGGCCCTTTTCCACAAACAGCCGCCCTCCTTGGCGCGGACCGGTAGAT  
 TCGTGGCAGAAAGATTGGATCAAACTGTGTCAACATATCAAGGCTACACTGGTGGCAGATCTGGTGGCGCAGG  
 CAGAGTCACCTTCTCAAGAGCAGCTGGTGACACAGGGAGGAGAGGGGAGACCCAGCCAGCTGTTGGAGATCT  
 TGTGTTCCCACTGTGCCCTCACGGGGCCAGGCATTGGCCCTGGGGCGGGAGTTCTGTCAAAGGAAGAGCCCTG  
 GGGCTGTGGGGCGTGTCTCCAGAGGAGACCCGGCAGCCGTTCTGAGCAGTGCAGAGAACATTGCTGTGGGGC  
 TTGCAACAGAGAAGGCTGTGCTTGGCTGTGAGCCAACTACAGCAGTGTATCAGGAGGAGGTGAAAGCAGCAG  
 TGAGTGCACACTTGTGAGCCAGGGTCTGAACTGCTGCCCGGGGGAGCGGAGGGGCTGCTCCCGGCCCTGAC  
 GTGCTCTCCTTGGCGCTGGGGCCACGGGACCTGACGAGGGAGTCTCCCAAGACATCTGGAACAGCTCCTAGGC  
 CAGTGGGCCAGACCTGCGGTGCCCGCAGTTCTGTGCCCACTGCTGAGCAGCATCTGGCAAGTGTCTGTGTG  
 GAGTAGCTTCCCTCTGCTGTGACATCAAAATTCCTATCTTAGGGCCCGCCAGCTACAGGCTGGAGAGAGG  
 CAGGCTCGAAGCTTCTGCACATGCTGCTTCTTGTGGAAGGAAGACTTTGAGGGCCGGTTCGCTGCAGCTG  
 CTGCTGAGCCCAAGAAATGTGGGCTTCTGGCAGACACAAGGCCAAGGGATGGGACTTCTGCTATTCTTGTCTA  
 CGGAGCTGGTGGAGAAGGGTCTGATGGGACGATGGAGATAGAGGCTGCTGCTGGCAGCCTCCACAGGCCCG  
 TGGCCAGGGGACTTGTGTAAGAATTAGCAACACTGTCTAATCTGTTTCTAGCGAGCCCCACTGTCGGAACCC  
 CAGCTAAGAGCTGTGAGTTGGTGAGCCAAACCGGGCAGCTGTGCTGGCCAGCTTGGGGTGAAGAGTGGCC  
 CTGCTCTGGGACTTGACACAGAACCTTGACCCCGGCTCACGAGGAGGCCAAGTGGCCAACTGCACGCCCTCAC  
 TGGTTGGGGTGTAGCTGGGTCTACAGTCAGACTTCTGCTCTAAGGGTGTGACTTGGCTGGCATCCCAACCGGCA  
 ATCTAGAGGAAGAGAGTTGGCTGATTGGGATTATGGCAGAAAGTCCAGAGATTGCCACGCTTGGAGTAGAA  
 GAGGTGGATTGTTTATCTCTTGGATACTAAATGAAATGAGGTGTGGGGCTGTGACACAGAAATCAAGCT  
 CATTTGCTATCCAGCATCTCTTAAACTTTGTAGTCTTGAATTCATGACAGAGGCAATGACTCTGCTCTAAC  
 TTATGAAGAAAGTTAAACATGAATCTTGGGAGTCTACATTTCTCTATCAGCAGGAGCTGGACTGGCATCTCCTT  
 ATAAATGCCTAACACAGGCCGGGTCTGTGGCTGTATCCAGCTACTCAGGAGGATGAGGAGGAGACTGCTTGAAC  
 CTGGAGGTGGAGGTGTGAGTGAGCCGAGGTGCGACCACTGCACTCCAGTCTGGGTAAACAGAGCGAGACTTCTAG  
 AAAAGGCTAAACAAAGATAGGTAGGACTCAACCAACTGAAACCTGACTTCCCCCTGTACCTTCAGCCCGT  
 TGCAGGTAGTAACCTTTGAGACCTTCTCCTGACCAGGGACCAAGCAGGAGCATTTAGAGCTTTTGAATAAA  
 CTGCTTTCTTTAAAAAAGGGGCGCGCCCTTT  
 TTTTTTTTTTTTTTTTTAAAAAGGGCTTTTATTAATAATCTCCCAACAGATGGCTCCTGCAATCTGCCACAGCTC  
 TGGGCGCTGCTGTGAGGGAAGGCCCTGTTTTCCCTGAGCGGGGCTGGCTTGTCCATGGGTCCGCGGAGCTG  
 CGCGTGTGGCGCCTGGCGTGTCTAGCTGCTTCTTGGCGGCAACAGCTGCGGGGTGTGGGGCACCGGG  
 AGCTAAGAGCAGGCTGTGGTGTGAGGGGTGAGGCTGTCTCTTAAACGACACCTCGAGGTGCTCCTGAGATGCTG  
 GTGCCACCTGAGTGGCAGGGGAGCAGCTGTGGCGGTGCTCCTTCTYAGGCGAGTCTCTGGGGAACCTAAGCTC  
 GGGCCCTCTTCTGAAGACCGGAGGATGGGTGGGTGTGGGGGACTCTGGGGAAATGGCTGAGGAGCTACGTGT  
 GAGAGGGGCGGGTGTGGCTGCAGCGGCTGAGGCGCTCTCCTGAGGCTCAGTTTCCCTTCCGTCTA  
 ATGAAGAATCATCGCTGTCCGGTGTCTCAGGGCTATTAGGACTTGCCTCAGGAAGTGGCTTGGACGAGGCTCAT  
 GTTATTTCACAACTGCTTCGCGAGTTGGCTTGGCCAGGCTCATGGAATGGCCATGCTCCTCTGCTGGTGGAG  
 GTCCGCTGGGAGTGGCAGCCAGGCGGGGCCAGGCTGCGCTGGGGGTGAGGAGGCGCCCGGGGAGG  
 CCTCAACGAAGTTGGCTCCCGCACACAGGCGAGGCGGGCTCCCGCCCGCCGCGCACCTCCCTGACG  
 GCGCGTAGACAACTGGAGTCCGCTTGGCTGCTGCGCAGCAGGTAGCCCTTGATGCACTGCGGACGCGG  
 TCGTCCGCGAGCTGGAAGCAGCGCCCTTCCACAGCACGAACGCGGTGCGCT

**FIGURE 32**

MCFLNKLLLLAVLGWLFQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNAPVVDQQLLYTC  
 CPYIGELRKLLASWVSGSSGRSGGFMRKITPTTTTSLGAQPSQTSQGLQAQLAQAFFHNQPP  
 SLRRTVEFVAERIGSNCKVHIKATLVADLVRQAESLLQEQLVTQGEEGDPAQLEILCSQL  
 CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL  
 IRREVKA AVSRTLRAQGFEPAAARGERRGCSRA

**Signal peptide:**

amino acids 1-18

**N-glycosylation site.**

amino acids 244-248

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 89-93

**Casein kinase II phosphorylation site.**

amino acids 21-25, 167-171, 223-227

**N-myristoylation site.**

amino acids 100-106, 172-178, 207-213

**Microbodies C-terminal targeting signal.**

amino acids 278-282



**FIGURE 33**

TCCCTTGACAGGTCTGGTGGCTGGTTCGGGGTCTACTGAAGGCTGTCTTGATCAGGAAACTG  
 AAGACTCTCTGCTTTTGCCACAGCAGTTCTCTGACAGTTCCTTGAGGTGTGAACCCACATCCC  
 TGCCCCAGGGCCACCTTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAAATG  
 AGTAGCAACAAGAGCAGCGGTGACGAGTGTTCGTGATCCTCTTTGCCCTCATCACCATCTCT  
 CATCTCTACAGCTCCAACAGTGCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCGGTA  
 GCCGCCGACCTGTCAACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCATTTCTCGGC  
 AACAGACACTGCCCTCTCGGTGCCACCAAGTGTGTGATTGTGACGAGCTCCAGCCACCTGCT  
 GGGCACCAAGCTGGGCCCTGAGATCGAGCGGGCTGAGTGTACAATCCGCATGAATGATGCAC  
 CCACCACTGGCTACTCAGCTGATGTGGGCAACAAGACCACCTACCGCGTCTGTGGCCCATTCC  
 AGTGTGTTCCGCGTGTGAGGAGGGCCCCAGGAGTTTGTCAACCGGACCCCTGAAACCGTGTT  
 CATCTTCTGGGGGCCCCGAGCAAGATGCAGAAAGCCCCAGGGCAGCCTCGTGCCTGTGATCC  
 AGCGAGCGGGCCTGGTGTTCCTCAACATGGAAGCATATGCCGTCTCTCCGGCCGCATGCGG  
 CAATTGACGACCTCTTCCGGGGTGAGACGGGCAAGGACAGGGAGAAGTCTCATTCGTGGTT  
 GAGCACAGGTGTTTACCATGGTGATCGCGGTGGAGTTGTGTGACCAAGTGCATGTCTATG  
 GCATGGTCCCCCACTACTGACGCCAGCGGCCCGCCTCCAGCGCATGCCCTACCACTAC  
 TACGAGCCCAAGGGGCGGACGAATGTGTACCTACATCCAGAATGAGCACAGTCGCAAGGG  
 CAACCACCACCGCTTCATCACCAGAAAAGGGTCTTCTCATCTGCGGCCACGCTGTATGGCA  
 TCACCTTCTCCCAACCCCTCTCGGACCTAGGCCACCCAGCCTGTGGGACCTCAGGAGGGTCAG  
 AGGAGAAGCAGCCTCCGCCCAGCCGCTAGGCCAGGGACCATCTTCTGGCCAATCAAGGCTTG  
 CTGGAGTGCTCTCCAGCCAATCAGGGCCTTGAGGAGGATGTATCTCTCCAGCCAATCAGGGCC  
 TGGGGAATCTGTGTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTTC  
 TTGTGCAGTCAGGGCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG  
 AGGCTAAGGACATGTCTCTTCCCATGAGGCCTTGGTTTCAAGCCCCAGGAATGGACCCCCCA  
 ATCACTCCCCACTCTGCTGGGATAATGGGGTCTGTCCCCAAGGAGCTGGGAACCTGGTGTG  
 CCCCCCAATTTCCAGCACCAAGAGAGAGATTGTGTGGGGTAGAAGCTGTCTGGAGGCC  
 GGCCAGAGAATTTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA  
 GGCTGGCATCCAGGTCTTGGCTCTGCCCTGAGACCTTGGACAAACCTTCCCCCTCTCTGGG  
 CACCCCTCTGCCCACACCAAGTTTCCAGTGGGAGTCTGAGACCTTTCCACCTCCCTACAA  
 GTGCCCTCGGGTCTGTCTCCCCGCTGTGGACCTCCAGCCACTATCCCTGTCTGGAAGGCT  
 CAGCTCTTTGGGGGCTGTGGGGTGACCTCCCCACCTCCTGGAAAACCTTAGGGTATTTTTGC  
 GCAAACCTCCTTAGGGTTGGGGGACTCTGAAGGAAACGGGACAAAACCTTAAGCTGTTTTCT  
 TAGCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGCCAGGCCCTCCTTTCTGCCCC  
 CTAGCAGGAGGTTTTCCAACTGTTGGAGGCGCTTTGGGGCTGCCCTTTGTCTGGAGTCA  
 CTGGGGGCTTCCGAGGCTCTCCCTCGACCCTCTGTCTGCTGGGATGGCTGTCTGGGAGCTGT  
 ATCAGCTGGGTTCTGTCCCTGGCTCTGTATCAGGCATTTATTAAAGCTGGGCGCTCAGTGG  
 GGTGTGTTGTCTCTCTCTCTCTGGAGCCTGGAAGGAAAGGGCTTCAGGAGGAGGCTGTGA  
 GGTGGAGGGACCATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGATGGGTGG  
 GGGCGGTGACTGCCACAGCTTGGTTTTGTAAATGATTTGTACAGGAATAAACACACCTACGC  
 TCCGGAAAAA

**FIGURE 34**

MSSNKEQRSVAVFVILFALITILLYSSNSANEVFHYGSLRGRSRRFPVNLKKWSITDGYVPIL  
 GNKTLPSRCHQCIVVSSSSHLGLGPEIERAECTIRMNDAPTGTYSADVGNKTTYRVVAH  
 SSVFVLRRLRPQEFVNRTPETVFIFWGPPSKMQKPGQSLVRVIQRAGLVFFNMEAYAVSPGRM  
 RQFDDLFRGETGKDREKSHSWLSTGWFTMVI AVELCDHVVHVGMPVFPNYCSQRPRLQRMPIH  
 YIEPKGPDECVTYIQNEHSRKGNNHHRFITEKRVFSSWAQLYGITFSPSWT

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 9-31 (type II)

**N-glycosylation site.**

amino acids 64-68, 115-119

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 50-54

**Casein kinase II phosphorylation site.**

amino acids 3-7, 29-33, 53-57, 197-201

**Tyrosine kinase phosphorylation site.**

amino acids 253-262

**N-myristoylation site.**

amino acids 37-43, 114-120, 290-294

## FIGURE 35

GTTTCCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAATAGGAACTCAGCGGACCGGGAGCGACGAGCTT  
 GAGGGAAGCATCCTAGCTGTGTGGCGCAGAGGGCGAGGCTGAAGCGAGGTGGCCCGAGGTGTCTGAGGGGCTGG  
 GGCANAAGTGAAGAGTTTCAAAACAAAGCTTCTCGAACCCATGACCCTGAAGTCTTGTGCACATTTATACCGT  
 CTCGAGGATACAGCTCGAATCTAGAAGAGTGGATTTGCCAGGGACCGGCATATCTCTTTGTGTGACCTTGGC  
 GGCCTATGGAGCTTGGCTTCAGACCTTTGTGATACACCTGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG  
 AGGCCTGAGGTCACATCGTGGCTGCTCTCTCTAGCCACAGCAGGCTGCTTGTGACTTGAACGAGGTCCCTCAG  
 CTCACCGTCCAGCTGGCTGCCCTCCACGCTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGGTGGTGAACCTCCA  
 AGATGAATGTAACTTCGAGCTGAATGGAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCTCTCATCACC  
 CAGGGGACCTCGTCATCTACTGCCCTTAACAACCACTCTGGGACGCTACAGTGTGGCCCGGATGCCCTGGC  
 GGGGCTGTGGGACGGTGGCCAGCACTGTGACATAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCAGCTG  
 ATTTGAAGTGGATGAGGGAACACAGCAGTCTATGCTGCCACCTGCCCTGAGAGCCACCCAAAGCCGAGGTCCGG  
 TACAGCTCTAAACAAAGAGTGGCTGGAGGCCCTCAGAGGTAACTACCTGATCATGCCCTCAGGGAACCTCCAGATT  
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCTTCAACCCAGTGACCCAGGAAGTGAAAAAC  
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCAGAGGCC  
 CAAACCATCATCGTCAACAAAGCCAGAGTCTCATTTGAGGATGTGTGGCCAGCTGGAATCCCCCCACCGGCT  
 ACCTGGGCCAAGATGGGTCCAGTGTACCGGCTACAAACAAAGACGGCTTCTGCTGAGCAACCTCTCATCGAC  
 ACCACAGCGAGGAGGACTCAGGCACCTACCGCTGCATGGCCGCAATGGGGTGTGGGACGCCCGGGAGCGGCT  
 ATCCTCTACAATGTCCAGTGTGTTGAACCCCTGAGGTACCATGGAGCTATCCAGTGTGTCTATCCCTCGGGC  
 CAGAGTGGCCAGCTTACCTGTGAGTGGTGGAGACCCCGGCTCCGCTGTGTGGCTGAGGAATGCTGTGTGCC  
 CTGATCTCCAGCCAGCGCTTCGGCTCTCCGACGGCCCTCGCGTGTGTGGCTGAGGAATGCTGTGTGCC  
 GTCTACACGAGCTGTCGCGAGGAGAGTGGAGCGCCCATCGGCTAGCTCAGCTGGGACCTCAGGCCAAGC  
 ATAACTCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCTGTATACACCTTCCAATCGGCAAC  
 CCTGAGCAGATGCTGGAGGGCAACCCGGCGCTCCGAGACCCCAACCTCAGTGGGGCTGCTTCCCCGAAGGT  
 CCAGGAGAAAGGGGACGGGGCTCCCGCCGAGGCTCCCATCATCTCAGCTCGCCCGGACCTCCAAGACAGAC  
 TCTATGAGATGGTGTGGCGGCTCGCATGAGGGCAGTGGCCGGGCGCCAACTCTACTATGTGGTGAACAC  
 CGCAAGCAGGTCACAAAATCTCTGACGATTTGGACCATCTCTGGCATTCCAGGCCAACGACCGCTGACCCCT  
 ACCAGCTTGACCCCGGGAGCTTGTATGAAGTGGAGTGGCAGCTTACAACCTGTGGGAGAGGGCCAGACAGCC  
 ATGGCTACCTTCCGAAGCTGGACGGCGGCCAAACCCGAGATCATGGCCAGAAAGAGCAGCAGATCCAGAGAGAC  
 GCGCTGGAGCCAGTCCCGACAGCGAGCCAGCCAGACCAAGCCGCGGCTCTCCCCCCAGGAGCTCCGACAGG  
 CCCACCATCTCCAGCGGCTCCGAGACCTCAGTGTACGCTGACCTGGATCCCCCTGGGAATGTTGGGTTCCCAATC  
 CAGTCTCTCGGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCGAGGCTCCCTCCCA  
 TCGCGGCTGCTCGGTGGAGATCAGCGGCTAGAGAAGGACACTCTCTACAAGTTTCGAGTCCGGGCTCCGACATG  
 CTGGGGAGAGCGAGCCCGAGCGCCCTCTCGGGCCTTACTGGTGTGAGGCTACAGCGTCTGAACATG  
 CCGCTGAGGCTCTTATATCACTCTCAGGATGGCGTCAATGAGCACCATCATGTCTCAAGTGGATGTACATG  
 CCAAGTAAGTACAACAACACCCCAATCCATGGCTTTTATATCTATTTACGACCCAGACAGCTGACAAATGATGT  
 GACTACAAGAAGGATATGTGGAAGGGGACAGTACTGGCACTCATGAGCCACTGAGCCAGGACCTCCATCG  
 CGAATTAAGTACGAGTGTCTCAATGAAGGAGGGAGAGGAGTTCAGCAACGATGATGATCTGTGAGACCAAGGT  
 GCGAAGTCTTCTGGCCAGCTGGTGCATGCCACCCCAACTCTGGCCGCGCCCTTCTGTGAAAC  
 ATAGAGCGGCGGGTGGGCACTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATGTGATTGTGGGGTGTG  
 CTGGGCTCCATGCTTCTATCATCTGTCACCTTCTATCCCTTCTGTGTGGAGGGCTGGTCTAAGCAAAAACAT  
 CCAACAGACCTGGGTTTTCTCGAAGTGGCTTCCACCTCTCGGCCGTATATGTTGGTGCATTGGGAGGACT  
 CAGGCGCCAGGCGCATGGACAGCCCTACTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG  
 AATAGGGGCTGCCCTCGGCTGAGTGGGCTACCCGGGCAAGCCCGACGAGCTGCCAGGCGAGCTTCAG  
 CAGCAGAGTGACACCCAGGCGCTGCTGAGCGAGCCCATCTTGGCAATGGATGTAGCCCCCAAGTCAACGATC  
 ACGAGGGGTCCCAAGTGTAGCCCGGAGCGAGGGCTCTTCTTATACACTTCCCGACCTCAATCAGTACG  
 CTGCGAGCCCATCAGCATGCTGCTGCCAACCGCAGGAGCGAGCTGCTGCTGCGGCTCAGGSGTGAAGAGAGCC  
 CCGCAGATCTCTCTCGTGAACAGCTGTGGACCCCTGCTCAATTCACAGGCGCCCATGCTGCTGGGCTTTGTG  
 CCACTTGAAGCTGGACACTGCTGACTCTCTCGCAAGTGAAGTGGAGAGACTGGTGTGCCAGACCCGCTGAGG  
 GCTTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCGGGGCACTGGCTGGTGTGCTTTTGAACACCACT  
 CTCACATTTAGGACGAGAGCTGATATCCAGAAAGACTATATATGTTTCTTTTAAAAAATAAGAGAAAAA  
 AGACAGCAGAAAAATGGTATTTATTTTCTATTATAGCCATATTTATATATTTATGCACTTTGTAATAAATGTA  
 TATGTTTATATATCTCGAGAGACATAAGAGTCTTACCGGTTGAGTTGGAGAGGAAAAATAAGAGACCTGCCA  
 CTTACAGGAGTCACTCCGAGGAAGACCCGACAGGCTGGCGGGACAGACTCTCAATCGGGGCTCTGCACTG  
 TGAGGCGAGGCTGCAAGGAGGCCACAGATAAGCTGGCAGAGGAAGGATCCAGGACCATGGTTCTATCAGAGCA  
 GCGGGGAACAGCAAGGGGACGGTATCACAGCTGGAGACCCCAACACAGATGGCTGGATCGGCTGCTACGGGAA  
 CAATTTTCTAAGATGCCATGAGACAGACCAAGATGTGACAGCACTATGAGCATTAATAAACCTTCCAGAT  
 CAATTAATCGTGGCAACATATCTCTGTAATAAACAAACACTGTAACTTCTAAATAAATGTTAGTCTTCCCTGAAAA

**FIGURE 36**

MLRGTMTAWRGMREVTLACLLLATAGCFADLNEVPQVTVQASTVQKPGGTIVILGCVVEPP  
 RMNVTVRLNGKELNGSDDALGVLI THGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL  
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMP SGNLQ  
 IVNASQDEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSL  
 ILECVASGI PPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGPQGA  
 AVILNVQVFEPPEVTMELSQLVIPWQSAKLTCEVRGNPPPSVLWLNRNAVPLISSQRLRLS  
 RRALRVLSMGPEDEGVYQCMANEVGSAAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSK  
 LGNPEQMLRGQPALPRPPTSVGPASPKCPGEKGQGAPAEAPIILSSPRTSKTDSYELVWRPR  
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE  
 GQTAMVTFTTGRPRKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASE  
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRV  
 RALNMLGESEPSAPSRPYVVS GYSGRVYERPVAGPYITFTDAVNETTIMLKWMIIPASNNNT  
 PIHGFYIYYRPTDSNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM  
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSIVL  
 IIVTFIPFCLWRAW SKQKHTTDLGFERSALPPSCPYTMVPLGGGLPGHQASGQPYLSGISGRA  
 CANGIHMNRGCPSSAAVGYPGMKPQQHCPGELQQQSDTSSLLRQTHLNGYDPQSHQITRGPK  
 SSPDEGSFLYTL PDDSTHQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDPPFHSG  
 PPCCGLGLVPVEEVDSPDSCQVSGGDWCPQHVPVGAYVGQEPGMQLSPGFLVRVVSFETPPLTI

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 16-30 (type II), 854-879

**FIGURE 37**

CGGGAGGCTGGGTCGTCATGATCCGGACCCCATTTGTCGGCCTCTGCCCATCGCCTGCTCCTC  
 CCAGGCTCCCGCGGCCGACCCCGCGCAAC**ATG**CAGCCACGGGCGCGAGGGTTCCTCGCGC  
 GCTCAGCCGGCGGTATCTGCGGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCTGCGGCAGC  
 CCGTAACCCGCGCGGAGACCACGCCGGGCGCCCCAGAGCCCTCTCCACGCTGGGTCCCCC  
 AGCCTCTTACCACGCCGGGTGTCCCCAGCGCCCTCACTACCCAGGCTCACTACGCCAGG  
 CACCCCCAAAACCTTGGACCTTTCGGGGTCGCGCGCAGGCCTGATGCGGAGTTTCCCACTCG  
 TGGACGGCCACAATGACCTGCCCCAGGTCCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT  
 GTTAACCTGCGAAATTTAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT  
 GGGTGCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAGACTGCCGTGCGCC  
 TCGCCCTGGAGCAGATTGACCTCATTACCGCATGTGTGCTCCTACTCTGAACCTCGAGCTT  
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTGNAGGG  
 TGGTCACTCACTGGACAGCAGCCTCTCTGTGCTGCGCAGTTTCTATGTGCTGGGGGTGCGCT  
 ACCTGACACTTACCTTCACCTGCAGTACACCATGGGCAGAGAGTTCACCAAGTTCAGACAC  
 CACATGTACACCAACGTGACGGATTGACAAGCTTTGGTGAGAAAGTAGTAGAGGAGTTGAA  
 CCGCCTGGGCATGATGATAGATTTGTCTATGCATCGGACACCTTGATAAGAAGGGTCCTGG  
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCCACTCAGCTGCCAGAGCTGTGTGTGACAATTTG  
 TTGAATGTTCCCGATGATATCCTGCAGCTTCTGAAGAACGGTGGCATCGTGATGGTGACACT  
 GTCATGGGGGTGCTGCAGTGCAACCTGCTTGCTAACGTGTCCACTGTGGCAGATCACTTTG  
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATCGGATTGGTGGAATATGACGGGACT  
 GGCCGGTTCCCTCAGGGGCTGGAGGATGTGTCCACATACCCAGTCTGATAGAGGAGTTGCT  
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTTCGTGGAAACCTGCTGCGGGTCT  
 TCAGACAAGTGGAAGGTGAGAGAGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTTT  
 CCATATGGGCAACTGAGCACATCCTGCCACTCCCACCTCGTGCTCAGAATGGACACCAGGC  
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATCGGGTCCCCTGGAGGTCTCAAATGCCT  
 CCCCATACCTTGTTCAGGCCTTGTGGCTGTGCCACCATCCCAACCTTCACCCAGTGGCTC  
 TGCT**TGA**CACAGTCGGTCCCCGAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCTCCT  
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGA AAA

**FIGURE 38**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLLLLLLLRQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTTPGLTTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSHGQ
TSLDRLRDGLVGAQFWSASVSCSQSQDQTAVRLALEQIDLIHRMCASYSELELVTSAEGLNSS
QKLACLIGVXGGHSLDSSLSVLRSFYVLGVRYLTLTFTTCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLSYASDTLIRRVLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEELQGVLRGNLLRVFRQVEKVREESRAQSPVEAEFPYQGLSTSCH
SHLVPQNGHQATHLEVTQPTNRPVWRSSNASPYLVPGLVAAATIPTFTQWLC
```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**Transmembrane domain:**

amino acids 313-331

**N-glycosylation sites.**

amino acids 119-122, 184-187, 243-246 and 333-336

**N-myristoylation sites.**

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 136-146

**FIGURE 39**

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA  
 TCCCTCTATGACTGCAATGTGAGGTGTCCGGCTTTGCTGGCCAGCAAGCCTGATAAGC**ATG**  
 AAGCTCTTATCTTTGGTGGCTGTGGTGGGTGTTTGTGGTGCCCCAGCTGAAGCCAACAA  
 GAGTTCTGAAGATATCCGGTGCAATGCATCTGTCCACCTTATAGAAACATCAGTGGGCACA  
 TTTACAACCAGAATGTATCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA  
 GTGCCTGGCCATGACGTGGAGGCCCTACTGCCTGCTGTGCGAGTGCAGGTACGAGGAGCGCAG  
 CACCACCACCATCAAGGTCATCATTGTCTACTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT  
 ACATGGCCTTCTTGATGCTGGTGGACCCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA  
 CTGCAACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG  
 GGGACCCCAGCAAAACACAGTCTTGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC  
 AAGTCAGGAGCAGCGGAAGACAGTCTTCGATCGGCACAAGATGCTCAGC**TAGAT**GGGCTGG  
 TGTGGTTGGGTCAAGGCCCCAACACCATGGCTGCCAGCTTCCAGGCTGGACAAAGCAGGGGG  
 CTACTTCTCCCTTCCCTCGGTTCCAGTCTTCCCTTTAAAGCCTGTGGCATTTTTCCCTCCTT  
 CTCCTAACTTTAGAAATGTTGTACTTGGCTATTTTGATTAGGGAAGAGGGATGTGGTCTCT  
 GATCTCTGTTGTCTTCTTGGGTCTTTGGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA  
 ATGGAGACATTCGAGGCGGCCTCAGGAGTGGATGCGATCTGTCTCTCCTGGCTCCACTCTTG  
 CCGCCTTCCAGCTCTGAGTCTTGGGAATGTTGTTACCCCTTGAAGATAAAGCTGGGTCTTCA  
 GGAACCTCAGTGTCTGGGAGGAAGCATGGCCAGCATTACAGCATGTGTTCCCTTCTGCAGTG  
 GTTCTTATACCACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG  
 AGGACAGCTCTGATGGGAGAGCTGGGCCCCCTGAGCCCACTGGGTCTTCAGGGTGCACTGGA  
 AGCTGGTGTTCGCTGTCCCTGTGCACTTCTCGCACTGGGGCATGGAGTGCCCATGCATACT  
 CTGCTGCCGCTCCCTCACCTGCATTGAGGGGTCTGGGCAGTCCCTCCTCTCCCCAGTGTG  
 CACAGTCACTGAGCCAGACGGTCGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA  
 CACCACAGCCCCGTACTTGGGTTGCCTCTTGTCCCTGAACCTTCGTTGTACCAGTGCATGGA  
 GAGAAATTTTGTCTCTTGTCTTAGAGTTGTGTGTAATCAAGGAAGCCATCATTAATTTG  
 TTTTATTTCTCTCA

**FIGURE 40**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHIYNQNVSQKDCNCLHVVEPM
PVPGHLDVEAYCLLCECRYEERSTTTIKVIVIVYLSVVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

**Important features:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 90-112

**N-glycosylation sites.**

amino acids 21-24, 38-41 and 47-50



**FIGURE 41**

AGCGGGTCTCGCTTGGGTTCGCGTAATTTCTGTCCTGAGCGGTGAGACTGAGTTTCATAGGGTCTGGGTCCCGGA  
 ACCAGGAAGGGTTGAGGGAACAACATCTGCAAGCCCGCGACCCCAAGTGAAGGGGCCCGTGTGGGGTCTCC  
 TCCCTTTGCATTTCCACCCCTCCGGGCTTTGGCGTCTCCCTGGGACCCCTCGCCGGGAGATGCGCCGCTGTGATG  
 CGGAGCAAGGATTGCTCCTGCTGCTGCTCCTACTGGCCCGCGGTGCTGATGGTGGAGAGCTCACAGATGGCGCAT  
 TCGCGGGCCAACTCAACTGACATCAAGTCTCTCTGGGCGGGGAGACGCCCTGGTCAAGGCCGCCAATCGATCTGCG  
 GGCATGTACCAAGGACTGGCATTCGCGCGGAGTAAGAAGGGGCAAAACCTGGGCGAGGCTACCCCTGTAGCAGT  
 GATAAGGAGTGTGAAGTGGGAGGTATTGCCACAGTCCCAACAGGATCATCGGCGCTCATGGTGTGTGCGGAGA  
 AAAAAAGAGCGCTGCCACGGAGATGGCATGTCTGCCCCAGTACCCGCTGCAATAATGGCATGTGATCCCGAGTT  
 ACTGAAAGCATCTTAACCCCTCACATCCCGCTCTGGATGGTACTCGGCACAGAGATCGAAACCAACGGTCATTAC  
 TCAAAACCATGACTTGGGATGGCAGAACTTAGGAAGACCACACACTAAGATGCACATATAAAGGGCGATGAAGGA  
 GACCCCTGCTACGATCATCAGACTGCATTGAAGGGTTTGTGTGCTCGTCATTTCTGGACCAAAATCTGCAAA  
 CCAGTGTCTCCATCAGGGGGAAGTCTGTACCAACCAACGCAAGAGGGTTCTCATGGGCTGGAAATTTTCCAGCGT  
 TGCAGTGTGCGAAGGGCCTGTCTGCAAAAGTATGGAAGATGCCACCTACTCCTCCAAAGCCAGACTCCATGTG  
 TGTGAGAAATTTGATCACCATTGAGGAACATCATCAATTGCAGACTGTGAAGTTGTATTTAATGCATTATAG  
 CATGGTGGAAATAAGGTTTCAGATCAGAGAAGATGGCTAAAATAAGAAACGATATAAGAAATATAGATGATCACA  
 AAAGGGAGAAAGAAACATGAACATGAATAGATAGAATGGGTGACAAATGCAGTGCAGCCAGTGTTCATTATG  
 CAACTTGTCTATGTAAATAATGTACACATTTGTGGAATAATGCTATTATTAAGAGAACAGCACACAGTGGAAATT  
 ACTGATGAGTAGCATGTGACTTTCCAAGGTTTAGGTTGTGCTGGAGGAGAGGTTTCTTCAGATTGCTGATTGC  
 TTATACAAATAAACCTACATGCCAGATTTCTATTCAACGTTAGAGTTTAAACAAATACTCCTAGATAAATCTGTTA  
 TACATAAGTTCTAAAAATAAATTTGCTAAACAAGAAATGAAACATGGAGCATTTGTTAATTTACACAGAAAAAT  
 TACCTTTGTATTCTTACAACACTCTCTGCTGTTCAATCAAGAGTCTTGGTATATGAAGAAAAAATCAGTCAATAT  
 TTCCAAATAATTTGCAAAATAATGGCCAGTTGTTTAGGAAGGCCCTTAGGAAGACAAATAAATAACAAACAGACAG  
 CCACAATACTTTTTTCAAATTTTAGATTTTACCTGTAATTAATAAGACTGATACAGAACCAAAACAGTTCC  
 TTCAGATTCTCCGAATGACAGATATATCTCTTTATCCTATGTGATTCCTGCTGATGACATTATATTTTCCA  
 AACTATACCCATAAATTTGTGACTAGTAAAATCTTTACACAGAGCAGAAATTTTACAGATGGCAAAATAATTTAA  
 GATGTCGAATATATTTGTGGAAAGAGGCTAACAGAGAGATCATTTATTTCTTAAGATTGGCCATTAACCTATATTT  
 GATAGAATTAGATTGGTAAATACATGTATTATACATATCTCTGTGGTAAAGAGACTTAAGCTGGATCTGACTG  
 CACTGGAGTAAGCAAGAAAAATGGGAAAACTTTTTCGTTTGTTCAGGTTTTTGGCAACACATAGATCATATGTCTG  
 AGGCACAAGTTGGCTGTTTCATCTTTGAAACCGAGGGGATGCACAGTCTAAATGAATATCTGCATGGGATTGCTAT  
 CATATAATTTTACTATGCAGATGAATTCAGTGTGAGGTCTGCTGCGTACTCCTCAAAATTTATTTATTTATAG  
 TGCTGAGATCCTCAAAATATCTCAATTTCAAGAGGTTTACAAAAATGTACTCCTGAAGTAGACAGAGTAGTGAGG  
 TTTCTATTGCCCTTATAAGCTTCTGACTAGCCAAATGGCATCATCCAAATTTTCTTCCCAACCTCTGCAGCATCTG  
 CTTTATTGCCAAAGGGCTAGTTTCGTTTCTGAGCCATTTGGGTTAAAAAATAAAGTAGGATACTTTGTAAA  
 ACCTGCATATTGCTAATCTATAGACACCACAGTTTCTAAATTTCTTGAACCACTTTACTACTTTTTTAAACCT  
 AACTCAGTTCTAAATACTTTTGTCTGGAGCACAACAAATAAAGGTTATCTTTATAGTCTGACTTTAAACCTTTT  
 TAGACCACAACTCAGTTTGTGATTTTCTTTTAACTTAATCCATCTGCAGTCTCAAATTTAAGTTTCTCCAGTAG  
 AGATTGAGTTTGAGCTGTATATCTATTAATAAATTTCAACTTCCACATATATTTACTAAGATGATTAAAGACTTA  
 CATTTTCTGCACAGGTCTGCAAAAACAAAAATTTAAACTAGTCCATCCAAGAACCAAGTTTGTATAAACAGGT  
 TGCTATAAGCTTGTGAATGAAAAATGGAACATTTCAATCAACATTTCTATATAACAATTTATATATTTACAAT  
 TTGGTTTCTGCAATATTTTCTTATGTCCACCTTTTAAAAATTTATTTTGAAGTAATTTTATTACAGGAATG  
 TTAATGAGATGATTTTCTTATAGAGATATTTCTACAGAAAGCTTTGACAGGAATATATTTGCAGCTATTGAC  
 TTTGTAATTTAGGAAAAATGTATAATAAGATAAATCTATTGAATTTTCTCCTCAAAAACTGAAAAAATAA  
 AAAAAA

**FIGURE 42**

MAALMRSKDSSCCLLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA  
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQSSACMVCRRKKKRCHRDGMCCPSTRCNN  
GICIPVTESILTPHIPALDGTNRHNRHGHYSNHDLGWQNLGRPHTKMSTIKGHEGDPCLRS  
SDCIEGFCCARHFWTKICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS  
SKARLHVCQKI

**Signal peptide:**

amino acids 1-25

**FIGURE 43**

TCTCAATCTGCTGACCTCGTGATCCGCCTGACCTTGTAATCCACCTACCTTGGCCTCCCAA  
 GTGTTGGGATTACAGGCGTGAGCCACCGCGCCGCCAACATCAGTTTTTAAAAATTGATT  
 TCTTCAAATTCATGGCAAATATTTCCCTTCCCTTTAACTTCTTATGTCAGAATGAGGAAGGA  
 TAGCTGCATTTATTTAGTCAGTTTTTCATTGCATAGTAATATTTTCATGTAGTATTTTCTAAG  
 TTATATTTTAGTAATTCATATGTTTTAGATTATAGGTTTTAACATACTTGTGAAAATACTTG  
ATGTGTTTTTAAAGCCTTGGGCAGAAATTCGTATTGTTGAGGATTGTCTTTTATCCCCCT  
 TTTAAAGTCATCCGTCCTTGCGCTCAGGATTGGAGAGCTTGACACCACCAAAATGGCAAACA  
 TCACCAGCTCCCAGATTTTGGACCAGTTGAAAGCTCCGAGTTTGGGCCAGTTTACCACCACC  
 CCAAGTACACAGCAGAATAGTACAAGTCACCCACAACTACTACTTCTTGGGACCTCAAGCC  
 CCCAACATCCCAGTCCCTCAGTCCTCAGTCATCTTGACTTCAAATCTCAACCTGAGCCATCCC  
 CAGTTCCTTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGCCAGGCAGTCACTGTTCCCTCCT  
 CCTGGTTTGGAGTCCTTTCTTCCAGGCCAAAACCTTCGAGAATCAACACCTGGAGACAGTCC  
 CTCCACTGTGAACAAGCTTTTGACGCTTCCAGCAGCACCATTGAAAATATCTCTGTGTCTG  
 TCCACCAGCCACAGCCCAAACACATCAAACCTTGCTAAGCGGCGGATACCCCCAGCTTCTAAG  
 ATCCCAGCTTCTGCAGTGGAATGCCTGTTTGCAGAGATGTCACAGGATTAAATGTGCAGTT  
 TGGGGCTCTGGAATTTGGGTGAGAACCTTCTCTCTCTGAATTTGGATCAGCTCCAAGCAGTG  
 AAAATAGTAATCAGATTCCCATCAGCTTGATTGCAAGTCTTTAAGTGAGCCTTTGAATACA  
 TCTTTATCAATGACCAGTGCAGTACAGAATCCACATATACAACCTCCGTCAATACCTCCTG  
 CAGTCTGACAAGCTCATCACTGAATTCGTAGTCCAGTAGCAATGTCTTCCCTTTATGACC  
 AGAGTTCTGTGCATAACAGGATCCCATACCAAAGCCCTGTGAGTTCATCAGAGTCAGCTCCA  
 GGAACCATCATGAATGGACATGGTGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG  
 CAGCAAGCTACTCTTGTCATGGCTGGTGCCAACCAACAGAGGAAGAGGATAGCTCACGTGA  
 TGTGGAACACACAGTGGTCAATGGCTCATTGTTAAAGCAGCCCTTTTGCTTTTTTGT  
 TTTTGGACCAGGTGTTGGCTGTGGTGTTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT  
 GGTGGTCTCATATTTCTTGCCTTAATCAGACTGCACCACAAGTGCAGCATACAGTATGCAT  
 TTTAAAGATGCTTGGGCCAGGCGGGTGGCTGATGCCATAATCCCAGTGCTTTGGGGGGCC  
 AAGGCAGGCAGATTGCCAAGCTCAGGAGTTTGAGACCACCTGGGCAACATGGTGAAACTC  
 TGTCTCTACTAAAATACGAAAACTAGCCGGGTGTGGTGGCGCGCTGCCTGTAATCCCAG  
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTTGGGCTACAAAGTGAGACTCC  
 GTCGAAAAAGA

**FIGURE 44**

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFGELAPPKMANITSSQILDQLKAPSLGQFTTT  
 PSTQQNSTSHPTTTTSWDLKPPTSQSSVLSHLDFKSQPEPSPVLSQLSQRQQHQSQAQVTVPP  
 PGLESFPSQAKLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQPPKHIKLAKRRIPPASK  
 IPASAVEMPGSADVTGLNVQFGALEFGSEFSLSEFGSAPSSSENSNQIPISLYSKSLSEPLNT  
 SLSMTSAVQNSTYTTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPIYQSPVSSSESAP  
 GTIMNGHGGGRSQQTLDISKYSSKLLLSWLVP TKQRKRIAHVMWKT PVGQWLIR

**Signal peptide:**

amino acids 1-24

**FIGURE 45**

GCCGAGTGGGACAAAGCCTGGGGCTGGGCGGGGGCC**ATG**GCGCTGCCATCCCGAATCCTGCT  
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG  
 ACGCGGGGCTGTACACCTGCAACCTGCACCATCACTACTGCCACCTCTACGAGAGCCTGGCC  
 GTCCGCCTGGAGTCAACGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA  
 GGTGCTGGCGGTGGCGCGGGCGCACCCGCGCTTCTGACCTGCGTGAACCGGGGCACGTGT  
 GGACCGACCGGCACGTGGAGGAGGCTCAACAGTGGTGCCTGGGACCGGCAGCCGCCCGGG  
 GTCCCGCACGACCGCGGGACCGCCTGCTGGACCTCTACGCGTCGGGCGAGCGCCGCGCTA  
 CGGGCCCCTTTTTCTGCGCGACCGCGTGGCTGTGGGCGCGGATGCCTTTGAGCGCGGTGACT  
 TCTCACTGCGTATCGAGCCGCTGGAGGTGCGCGACGAGGGCACCTACTCCTGCCACCTGCAC  
 CACCATTACTGTGGCCTGCACGAACGCCGCTTCCACCTGACGGTCGCCGAACCCACGC  
 GGAGCCGCCCCCGGGGCTCTCCGGGCAACGGCTCCAGCCACAGCGCGCCCCAGGCCACG  
 ACCCCACACTGGCGCGGGCCACAACGTCAATGTATCGTCCCCGAGAGCCGAGCCAC  
 TTCTTCCAGCAGTGGGTACGTGCTGGCCACGCTGCTGCTCTTATCCTGCTACTGGTCAC  
 TGTCTCTTGCCGCCCGCAGGCGCCGCGAGGCTACGAATACTCGACACAGAAGTCGGGAA  
 AGTCAAAGGGGAAGGATGTTAACTTGGCGAGTTTCGCTGTGGCTGCAGGGGACACAGATGCTT  
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACAACATCCTGAAGGAGAGGGCGAGCT  
 GGCCACAGCCCCCTGCCTGCCAAGTACATCGACCTAGACAAAGGGTTCGGAAGGAGAACT  
 GCAAA**TAG**GGAGGCCCTGGGCTCCTGGCTGGGCCAGCAGCTGCACCTCTCCTGTCTGTGCTC  
 CTCGGGCATCTCCTGATGCTCCGGGGCTCACCCCCCTTCCAGCGGCTGGTCCCGCTTTCCT  
 GGAATTTGGCCTGGGCGTATGCAGAGGCGCCTCCACACCCCTCCCCAGGGGCTTGGTGGC  
 AGCATAGCCCCACCCCTGCGGCCTTTGCTCAGGGTGGCCCTGCCACCCCTGGCACAACC  
 AAAATCCACTGATGCCATCATGCCCTCAGACCCTTCTGGGCTCTGCCGCTGGGGGCTG  
 AAGACATTCTGGAGGACACTCCCATCAGAACTGGCAGCCCCAAAACCTGGGGTCAGCCTCA  
 GGGCAGGAGTCCCACTCCTCAGGGCTCTGCTCGTCCGGGGCTGGGAGATGTTCTGGAGGA  
 GGACACTCCCATCAGAACTTGGCAGCCTTGAAGTTGGGGTCAAGCCTCGGCAGGAGTCCCACT  
 CCTCTGGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCACCATGTGGGACTCCAG  
 GCACCATCTGTTCTCCCCAGGACCTGCTGACTTGAATGCCAGCCCTTGCTCCTCTGTGTTG  
 CTTTGGGCCACCTGGGGCTGCACCCCTGCCCTTCTCTGCCCATCCCTACCTAGCCTTG  
 CTCTCAGCCACCTTGATAGTCACTGGGCTCCCTGTGACTTCTGACCTGACACCCCTCCCTT  
 GGACTCTGCTGGGTGGAGTCTAGGGCTAGGAGTACATTTGGCTTCTGTACTGGCTGAGGA  
 CAGGGGAGGGAGTGAAGTTGGTTGGGGTGGCCTGTGTTGCCACTCTCAGACCCACATTT  
 GCATCTGCTGTTGGACCTGCCACCATCACAATAAAGTCCCCATCTGATTTTTAAAAA  
 AAAAA

**FIGURE 46**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTD RHVEEAQQVVHWDRQPPGVPHDRADRLDL
YASGERRAYGPLFLRDRVAVGADAFERGD FSLRIEPLVADEGTYSCHLHHHYCGLHERRVF
HLTVAEPHAEPPIRGSPGNGSSHSGAPGPDPTLARGHNVINVIVPESRAHFFQQLGYVLATL
LLFILLLVTVLLAARRRRGGYEYSDQKSGKSKGKDVNLAEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPAPKYIDLKGFRENCK

```

**Important features:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 237-262

**N-glycosylation site.**

amino acids 205-208

**Cell attachment sequence.**

amino acids 151-154

**Coproporphyrinogen III oxidase proteins.**

amino acids 115-140

**FIGURE 47**

CGCCGGAGGCAGCGCGCGCTGGCGCAGCGGCGAC**ATG**GCGCTTGCTCTCAGAGGACGACTTT  
 CAGCAGACTTCAAACCTCCACCTACGGAACCACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC  
 ACTGCTTGAGAAAGCTGCTGGACCGCCGCCCTGGCTGCAGAGGCCGAGGACCGCTTCT  
 GTGGCACATACATCATCTTCTTCAACCTGGGCATTGGCAGTCTACTGCCATGGAACCTCTTT  
 ATCACTGCCAAGGAGTACTGGATGTTCAAACCTCCGCAACTCCTCCAGCCCAGCCACCGGGGA  
 GGACCTTGAGGCTCAGACATCCTGAACCTACTTTGAGAGCTACCTTGCCGTTGCCTCCACCG  
 TGCCCTCCATGCTGTGCTGGTGGCAACTTCTGCTTGTCAACAGGGTTGCAGTCCACATC  
 CGTGTCTGGCCTCACTGACGGTCACTTGGCCATCTTCACTGGTGTAACCTGCAGTGGTGAA  
 GGTGGACACTTCTCCTGGACCCGCTGGTTTTTTTGGCGGTCAACATTGTCTGCATGGTGATCC  
 TCAGCGGTGCCTCCACTGTCTTCAACGAGCATCTACGGCATGACCGGCTCCTTTCTATG  
 AGGAACCCCCAAGCACTGATATCAGGAGGAGCCATGGCGGGACGGTCAGCGCCGTGGCCTC  
 ATTTGGTGACTTGGCTGCATCCAGTGATGTGAGGAACAGCGCCCTGGCCTTCTTCTGACGG  
 CCACCATCTTCTCCTGTCTGTCATGGGACTTACCTGCTGCTGTCCAGGCTGGAGTATGCC  
 AGGTACTACATGAGGCTGTTCTTGGCGCCATGTGTTTTCTGGTGAAGAGGAGCTCCCCA  
 GGACTCCCTCAGTGCCCTTTCGGTGGCCTCCAGATTATTGATTTCCACACACCCCTCTCC  
 GCCCCATCTGAAGAAGACGGCCAGCCTGGGCTTCTGTGTACCTACGTCTTCTTATCACC  
 AGCCTCATCTACCCCGCGTCTGCACCAACATCGAGTCCCTCAACAAGGGCTCGGGCTCACT  
 GTGGACCACCAAGTTTTTCTATCCCTCACTACCTTCTCCTGTACAACCTTTGCTGACCTAT  
 GTGGCCGGCAGCTCACCGCTGGATCCAGGTGCCAGGGCCCAACAGCAAGCGCTCCCAGGG  
 TTCGTGCTCCTCCGACCTGCCTCATCCCTCTTCTGTGCTCTGTAACTACAGCCCGCGT  
 CCACCTGAAGACTGTGGTCTTCCAGTCCGATGTGTACCCCGCACTCCTCAGCTCCCTGTGG  
 GGCTCAGCAACGGCTACCTCAGCACCTGGCCCTCCTACGGGCTTAAGATTGTGCCAGG  
 GAGCTGGCTGAGGCCACGGGAGTGGTGATGTCTTTATGTGTCTTGGGCTTAACACTGGG  
 CTCAGCCTGCTTACCTCCTGGTGCACCTCATCT**AGA**AAGGAGGACACAAGGACATTGGTG  
 CTTAGAGCCTTTGAAGATGAGAAGAGAGTGCGAGGAGGCTGGGGCCATGGAGGAAAGGCC  
 TAAAGTTTCACTTTGGGACAGAGAGCAGAGCACACTCGGGCTCATCCCTCCCAAGATGCCA  
 GTGAGCCACGTCCATGCCATTCCGTGCAAGGCAGATATTCCAGTCATATTAACAGAACCT  
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTTACAGCTGATGGTTA  
 ACATTCCACCTTCTTCTAGCCCTTCAAAGATGCTGCCAGTGTTGCGCCTAGAGTTATTACA  
 AAGCCAGTGCCAAAACCCAGCCATGGGCTCTTTGCAACCTCCAGCTGCGCTCATTTCCAGCT  
 GACAGCGAGATGCAAGAAATGCTCAGCTCTCTTACCTGAAGGGGTCTCCCTGGAATGGA  
 AGTCCCTTGGCATGGTCACTCCTCAGGCCCAAGACTCAAGTGTGCACAGACCCCTGTGTTCT  
 GCGGGTGAACAACCTGCCCACTAACAGACTGGAAACCCAGAAAGATGGGCTTCCATGAAT  
 GCTTCATTCCAGAGGGACAGAGGGCCTCCTGTGCAAGGGATCAAGCATGTCTGGCCTGGG  
 TTTTCAAAAAAGAGGATCCTCATGACCTGGTGGTCTATGGCTGGGTCAAGATGAGGGTC  
 TTTAGTGTTCTGTTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAATACTTGC  
 GTATTCAAAA

**FIGURE 48**

MAVVEDDFQHSSNSTYGTSSSLRADQEALLEKLLDRPPPGLRPEDRFCGTYIIFFSLGI  
 GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLAVASTVPSMLCLVANFL  
 LVNRVAVHIRVLASLTIVILAI FMVITALVKVDTSSWTRGFFAVTIVCMVILSGASTVFSSSI  
 YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVNRNSALAFFLTATIFLVLCMGly  
 LLLSRLEYARYYMRPVLAHVFSGEEELPQDSLAPSASRFIDSHTPPLRPILKKTASLGF  
 CVTYVFFITSLIYPVACTNIESLNKGSGSLWTTKFFIPLTTFLLYNFADLCGRQLTAWIQVP  
 GPNSKALPGFVLLRTCLIPFLVLCNYQPRVHLKTVVFQSDVYPALLSSLLGLSNGYLSTLAL  
 LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

**Transmembrane domain:**

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,  
 305-330, 448-472



**FIGURE 49**

**FIGURE 50**

MAPLALHLLVLPILLSLVASQDWKAERSQDPFEKCMQDDPDYEQLLKVVVTWGLNRTLKPQRV  
IVVGAGVAGLVAAKVLSDAGHKVTILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRIL  
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKL RN YVVEKVPEKLG YALRPQEKGHSPEDIYQMA  
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSRPAVQLLGDMSEDGFFYLSFAEALR  
AHSCLSDRLQYSRIVGGWDL LPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQIETSPPARNL  
KVLKADVLLTASGPAVKRITFSPPLPRHMQEALRLRHYPATKVFLSFRPPFWREEHIEGG  
HSNTDRPSRMI FYPPPREGALLASYTWS DAAAAFAGLSREEALRLALDDVAALHGPVVRQL  
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIYFAGEHTAYPHGWVETAVKS  
ALRAAIKINSRKG PASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQQLSLQ  
NTTHTRTSH

**Signal peptide:**

amino acids 1-21

# FIGURE 51

CTGACATGGCCTGACTCGGGACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCGGGCCTTCTGCCTGCAT  
 GAGCGCTCTGAAGACCCACCTGTCTCTGGAGGAACACGAGCGAGGGAAGAGACAGGGACTCGTGTGGCAGGAA  
 GAATCTCAGAGCCGGGAAGCCCCATTTCACTAGAAGCACTGAGAGATGCGGGCCCCCTCGCGAGGCTCTGAATTTCT  
 GCTGCTGTTTACAAAGATGCTTTTATCTTTAACTTTTTGTTTTCGCCACTTTCGCCACCCCGGGTGTGATCTGCAT  
 CTTGACATTTGGAGCTGCCATCTTCTTGTGGCTGATCACCAGACCTCAACCCTCTTAACTCTTCTTGACCTGAA  
 CAATCAGTCTGTGGGAATTTAGGGGAGGAGCAGGGAAGGGGGTTTCCGAGAAGAACATGACCTAACAAAGTTGCTG  
 CTCTCAGATGCCAGACTATGTATGAGGTTTCCAAAGAGGACTCGCTGTGTCTGACAATGGGCCCCCTGCTTGGG  
 ATATAGAAAACCCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGTCTGATAGACAGAGTACCTGGGTTT  
 CTGTCTCTGCATAAAGGCTTTATAAATCATCACCAGACCAATTTGTCCGCATCTTGTCTCAGAATAGGCCAGAGTG  
 GATCATCTCCGAATTTGGCTTGTACAGTACTCTATGTTAGCTGTACCTCTGTATGACACCTTGGGACCAGAGC  
 CATCGTACATATTTGTCAACAAGGCTGATATCGCCATGGTGATCTGTGACACACCCCAAAGGCATTGGTGTGAT  
 AGGGAATGTAGAGAAAGGCTTCAACCCGAGCCTGAAGGTGATCATCCTTATGGACCCCTTTGATGATGACCTGAA  
 GCAAAGAGGGGAGAGAGTGGAAATGAGATCTTATCCCTATATGATGCTGAGAACCTAGGCAAGAGACATTCAG  
 AAAACCTGTGCCTCTAGCCCAAGAGACCTGAGCGTCTATGCTTCAACAGTGGGACCACAGGTGACCCCCAAGG  
 AGCCATGATAACCCATCAAAATATTGTTTCAAATGCTGCTGCTCTTCAAAATGTGTGGAGCATGCTTATGAGCC  
 CACTCTGATGATGTGGCCATATCTACCTCCCTCTGGCTCATATGTTTGAAGAGATTTGACAGGCTGTTGTGTA  
 CAGCTGTGGAGCCAGAGTTGGATTCTTCCAAGGGGATATTCGGTTGCTGGCTGACGACATGAAGACTTTGAAGCC  
 CACATGTTTCCCGGGTGCTCGACTCCTTAAACAGGATCTACGATAAGGTACAAATAGGGCCAAAGACACCCCT  
 GAAGAAGTCTTGTGTGAAGCTGGCTGTTTCCAGTAAATCAAAGAGCTTCAAAGGGTATCATCAGGCATGTAG  
 TTTTGGGCAAGCTCATCTTTTGAAGATCCAGGACAGCTGGGCGGAAGGGTTCGTGTAAATGTCACTGGGCT  
 TGCCCCCATGTCACCTCAGTCATGACATTTCTCCGGGACGACATGGGATGTGAGTGTGAAGCTTTATGGTCA  
 AACAGAATGCACAGGTGGCTGTACATTTACATTTACCTGGGACTGGACATCAGTCACTTGGGGTCCCCCTGGC  
 TTGCAATTAAGTGAAGCTGGAGATGTGGCTGACATGAACACTTTACAGTGAATGAAGAGAGGTCTGCAT  
 CAGGGTGTCAAACGTTTCAAAGGATACCTGAAGGACCTGGAAGAGACACAGGAAGCCCTGGACAGTGATGGCTG  
 GCTTCCACAGGAGACATTTGGTCTGGCTCCCGAATGGAATCTGAAGATCATCGACCGCTAAAGAGAACATTT  
 CAGCTGACCCGAGAGGAATACATTTGCACCAGAGAGATAGAAAATATCTACACAGGAGTCAACCAAGTGTACA  
 AATTTTGTACACGGGGAGAGCTTACGGTCACTCTTAGTAGGAGTGGTGGTTCTGACACAGATGTACTTCCCC  
 ATTTGAGCCAGAGCTTGGGTGAAGGGCTCTTTGAGGAACCTGTGCCAAAACCAAGTTGTAAAGGAAGCACTTT  
 AGAGACTTGCAGAAAATTTGGGAAGAAAGTGGCTTAAACATTTTGAACAGGTCAAAGGCATTTTCTTCTATCC  
 AGAGCCATTTCCATTTGAAAATGGGCTCTTGACACCAACATTTGAAGCAAAAGCGAGGAGAGCTTCCAAAATCT  
 TCGGACCCAAATGACAGCTGTATGAGCACATCCAGGATAGGATAAGGTACTTAAGTACCTGCCGGCCACTG  
 TGCACTGCTTGTGAGAAAATGGATTAAAAACTATTCTTACATTTGTTTGGCTTCTCCTATTTTTTTTAAAC  
 TGTTTAACTCTAAAGCCATAGCTTTGTTTATATTTAGACATATAATGTGTAACCTTAGTTCCCAATAAATCA  
 ATCTGTCTTTCCCATCTTCGATGTTGCTAATATTAAGGCTTCAGGGCTACTTTTATCAACATGCCTGTCTTCA  
 GATCCAGTTTATGTCTGTGCTTCTCATGATTTCCAACTTAACTACTATTAGTAACCAAGTTCAGGGGT  
 CAAAGGGACCTCTGTGCCCTCTTCTTTGTTTGTATAAACATAACTTGCCACAGTCTCTATGCTTATTTACA  
 TCTTCTACTGTTCAAACCTAAGAGATTTTAAATTTCTGAAAACTGCTTACAATCATGTTTCTAGCCACTCCAC  
 AAACCATAAAATTTAGTTTATAGCTATCACTCATGTCAATCATATCTATGAGACAAATGTCTCCGATGCTCTT  
 CTGCGTAAATTAATTTGTACTGAAGGGAAGTTTGTATCATCAACCAATTTCTCTAACTCTCTAGTTAGATA  
 TCTGACTGGGAGTATTAATAATGGGCTTATGACATCTGTCCAAAAGGAATGCTGTTCTTAAAGCAITATTTA  
 CAGTAGGAACCTGGGAGTAAATCTGTTCCTACAGTTTGTGCTGAGCTGGAAGCTGTGGGGAGAGGATGTACA  
 GTGGGGCCAGTGAACTTTCCAGTAAATGAAGCAAGCACTGAATAAAAAAAGCTTGAATGGGAAACAAAGATCT  
 ACAGGCAAGCAGATGCCACACACAGGCTTATTTCTGTGAAGGAACCACTGATCTCCCCACCCCTTGATT  
 AGATTCTCTGCTTCACTTACCCACAGATAACACATGTTGTTTCTACTTGTAAATGTAAAGTCTTTAAATAAAC  
 TATTACAGATAAAAAA

**FIGURE 52**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775  
<subunit 1 of 1, 739 aa, 1 stop  
<MW: 82263, pI: 7.55, NX(S/T): 3  
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN  
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARKGVSQKNNDLTS  
CCFSDAKTMYEYVQFQRLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS  
PDQFVGIFAQNRPEWIISELACYTYSMVAVPLYDTLGPFAIVHIVNKADIAMVICDTPQKAL  
VLIGNVEKGFTPSLKVIIIMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED  
LSVICFTSGTTGDPKGAMITHQNIIVSNAAAFLKCEHAYEPTPDDVAISYLP LAHMFERIVQ  
AVVYSCGARVGGFQGDIRLLADDMLTKPTLFPAPVRLNRIYDKVQNEAKTPLKKFLLKLA  
VSSKFKEKQKGIIRHDSFWDKLI FAKIQDSLGGRRVIVTGAAPMSTSVMTFFRAAMGCQVY  
EAYGQTECTGGCTFTLPGDWTSGHVGVP LACNYVKLEADVADNMNYFTVNNEGEVCIKGTNVFK  
GYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKII DRKKNI FKL AQGEYIAPEK IENIYNR  
SQPVLQIFVHGESLRSSSLGVVVPD TDVLP SFAAKLGVKGSFEELCQNQV VREAILEDLQKI  
GKESGLKTFEQVKAIFLHPEPFSSIENGLLTPTLKA KRGE LSKYFRTQIDSLYEHIQD

**Important features:****Type II transmembrane domain:**

amino acids 61-80

**Putative AMP-binding domain signature.**

amino acids 314-325

**N-glycosylation site.**

amino acids 102-105, 588-591 and 619-622

**FIGURE 53**

GGAGGCGGAGGCCGCGGGCGAGCCGGGCCGAGCAGTGAGGGCCCTAGCGGGGGCCCGAGCGGGG  
 CCCGGGGCCCTAAGCCATTCTGAAGTCATGGGCTGGCCAGGACATTGGTGACCCGCCAAT  
 CCGGTT**ATGG**AGCACTGGAAAGCCAGCCCCCTCATCAAGCCCTTTGGGGCTCGGAAGAAGCGG  
 AGCTGGTACCTTACCTGGAAGTATAAACTGACAAACCAGCGGGCCCTGCGGAGATTCTGTCA  
 GACAGGGGGCCGTGCTTTTCTCTGCTGGTGACTGTCATTGTGTCATATCAAGTTGATCCTGGACA  
 CTCGGCGAGCCATCAGTGAAGCCAAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC  
 CTAGGGCCGCTGGAGCCCCACGGCGCAGAGGCAGTGGTCCCCGGCGGGTCTGGACGTAGA  
 GGTGTATTCAAGTCGACGAAAGTATATGTGGCAGTGGATGGCACCACGGTGCTGGAGGATG  
 AGGCCGGGAGCAGGGCCGGGGCATCCATGTCATTGTCTCAACCAGGCCACGGGCCACGTG  
 ATGGCAAAACGTGTGTTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGCTATTCTC  
 CAACATGGTAGCGCCCGGCCGAGTGCTCATCTGCATGTCAAGGATGAGGGCTCCTTCCACC  
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGGCAGCCAGGCTGGCCCTGCCCTGGGC  
 TGGAGGGACACATGGGCCTTCGTGGGACGAAAAGGAGGTCTGTCTTCGGGGAGAAACATT  
 TAAATCACCTGCCCTCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA  
 GCTCAGCAGAAGAGGCAGAGTGCCACTGGGCAGACACAGAGCTGAACCGTCGCCCGCGGGCGC  
 TTCTGCAGCAAAAGTTAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCACACCCATCGA  
 GTTTCAGCCTGACCCACTCCGAGACAACAGGCTCTCAATGTGCGCTGTGGCTGTCAATGTCAG  
 GGAACCGACCAATTACCTGTACAGGATGCTGCGCTCTCTGCTTTAGCCGAGGGGGTGCTCT  
 CCTCAGATGATAACAGTTTTCATTGACGGCTACTATGAGAACCCATGAGATGCTGGTGCAT  
 GTTTGGTCTGAGGGGCATCCAGCATACTCCCATCAGCATCAAGAAATGCCCGCTGTCTCAGC  
 ACTACAAGGCCAGCTCACTGCCACTTCAACCTGTTTCCGAGGGCCAAGTTTCTGTGGTT  
 CTGGGAAGAGGACCTGGACATTGCTGTGGATTTTTCAGTTTCTGAGCAATCCATCCACCT  
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTCTGCCGTGAATGACCAGGGGTATGAACACA  
 CGGCTGAGGACCCAGCACTACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC  
 AGGAGTCTCTGTACAAGGAGGAGCTTGAGCCCAAGTGGCTTACACCGGAAAAGCTCTGGGA  
 TTGGGACATGTGGATGCGGATGCCTGAACAACGCCGGGGCCGAGAGTGATCATCCCTGACG  
 TTTCCCGATCTACCACTTTGGCATCGTCGGCCTCAACATGAATGGCTACTTTCAAGAGGCC  
 TACTTCAAGAAGCACAAGTTCAACACGGTTCCAGGTGTCCAGCTCAGGAATGTGGACAGTCT  
 GAAGAAGAAGCTTATGAAGTGAAGTTCACAGGCTGCTCAGTGAGGCTGAGGTTCTGGACC  
 ACAGCAAGAACCCTGTGAAGACTCTTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC  
 TTTATTCGAATGGAGAAAGATGATGACTTCAACACCTGGACCCAGCTTGCCAAGTGCTCCCA  
 TATCTGGGACCTGGATGTGCGTGGCAACCATCGGGGCTGTGGAGATTGTTTCGGAAGAAGA  
 ACCACTTCTTGGTGGTGGGGTCCCGGCTTCCCCCTACTCAGTGAAGAAGCCACCTCAGTC  
 ACCCCAAATTTCTGGAGGCCACCCCCAAGGAGGAGGAGGCCACAGGAGCCCCAGAACAGAG  
**ATGA**GACCTCTCCAGACCTTGCGGGCTGGGTACTGTGTACCCCAAGGCTGGCTAGCCCT  
 TCCCTCCATCCTGTAGGATTTTGTAGATGCTGGTAGGGGCTGGGGCTACCTTGTTTTTAACA  
 TGAGACTTAATTACTAACTCCAAGGGGAGGGTTCCCTGCTCCAACACCCCGTTCTGAGTT  
 AAAAGTCTATTATTTACTTCTCTTGTGGAGAGGGCAGGAGAGTACCTGGGAATCATTACG  
 ATCCCTAGCAGCTGCTGCCCTTTGAATACCTCACTTTCCAGGCCCTGGCTCAGATCTCA  
 ACCTATTATTGACTGTCTGAGGGCTTGAAACAGGCCGAACCTGGAGGCGCTGGATTTC  
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGGCTGGCTCTTACTCAGGAACTGCTGTGCC  
 CAACCCATGGACAGGCCAGCTGGGGCCACATGCTGACACAGACTCACTCAGAGACCCCTTA  
 GACACTGGACAGGCCCTCTCTCAGCCTTCTCTTTGTCCAGATTCCAAGCTGGATTAAGTT  
 GGTCAATTGATTAAAAAAGAGAAGCCCTCTGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 54**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
MDDWKPSPLIKPFGARKKRSWYLTWKYKLTNQRALRRFCQTGAVLFLLVTIVIVNIKLILDTR
RAISEANEDPEPEQDYDEALGRLEPPRRRSGPRRVLDVEYSSRSKVYVAVDGGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPHEDEAMVLFILNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDWTAFVGRKGGPVFGEKHSKSPALSSWGDVPVLLKTDVPLSS
AEEAECHWADTELNNRRRRRFCskVEGYGSVCCKDPTPIEFSPDPLPDNKVLNVPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITVFIDGYEEPMDDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPFAKFAVVLEEDLDIAVDFFSFLSQSIHLEEDDSLYCISAWNDAQGYEHTA
EDPALLYRVETMPGLGWVLRRLSYKEELEPKWPTPEKLWDWDMWMMRPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKKHKFNTPVPGVQLRNVDLSLKKEAYEVEVHRLLSAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDDFTTWTQLAKCLHIWDLVVRGNHRLGLRFLFRKKNH
FLVVGVPASPSYSVKPPPSVTPIFLEPPPKKEGAPGAPEQT

```

**Important features of the protein:****Transmembrane domain:**

amino acids 38-55

**Homologous region to Mouse GNT1**

amino acids 229-660

**FIGURE 55**

CGGACGCGTGGGCTGCTGGTGGGAAGGCCATAAGAAGCTGGAAGGCCACTCTCTTGGAAACCACCACAC  
 CTGTTTTAAAGAACCTAAGCACCATTAAAGGCCACTGGAATTTGTTGTCTAGTGGTTGTGGGTGAATA  
 AAGGAGGGCAGAA**ATGGAT**GATTTTCATCTCCATTAGCCTGCTGCTCTGCGCTATGTTGGTGGGATGTTA  
 CGTGGCCGGAATCATTTCCCTTGGCTGTTAATTTCTCAGAGGAACGACATGAAGCTGGTGACATGTTTTGG  
 GTGCTGGCCCTTCTCTGTGGAAGTGTCTGGCAGTCATCGTGCCTGAAGGATACATGCCCTTTATGA  
 GATATTTCTGAGGGAAAAACCAAGCAAGCAAGTGAACACATATGTGATTTGCATCAGACAAAGCAGC  
 AGAAAAATCAGTTGTCCATGAACATGAGCAGACGCCACGACCACACAGATGCATGCCCTATATTGGTG  
 TTTCCCTCGTTCTGGGCTTCGTTTTTCATGTGTCTGGTGGACAGATTGGTAACCTCCATGTGCATTCT  
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAAAATCACCACCACGCTGGGTCTGGTTGTCCA  
 TGCTGCAGCTGATGGTGTGCTTTGGGAGCAGCAGCATCTACTTCACAGACCAGTGTCCAGTTAATTG  
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTTTGGACTGGTTTCCTTCTTGATGCATGCT  
 GGCTTAGAGCGGAATCGAATCAGAAAGCACTTGCTGGTCTTTGCATTGGCAGCACCAGTTATGTCCAT  
 GGTGACATACCTTAGGACTGAGTAAGAGCAGTAAAGAAGCCCTTCAGAGGTGAACGCCACGGGAGTGG  
 CCAATGCTTTTTCTCTGCCGGGACATTTCTTTATGTTGCCACAGTACATGTCTCCCTGAGGTGGCGGA  
 ATAGGGCACGCCACAAGCCGATGCCACGGGAGGGAGAGCCCTCAGCCGCTGGAAGTGGCAGCCCT  
 GGTTCGGGTTGCCCTCATCCCTCTCATCTGTCTAGTAGGACACGAGCAT**TAAAT**GTTCAGGCTCCAGC  
 CTTGGTCCAGGGCCGTTTTGCCATCCAGTGAGAACAGCCGGCAGCTGACAGCTACTCACTTCCCTGATC  
 TTTGCTCTCACCCTTGGCAGCTCTCATCATGTATTCCTAGAGTCCAGAGGGAGGTGAGGTTAAACCTG  
 AGTAATGGAAAGCTTTTAGAGTAGAAACACATTTACGTTGCAGTTAGCTATAGACATCCCATTTGTGT  
 TATCTTTTAAAGGCCCTTGACATTTTGCCTTTTAAATATTTCTTAAACCTATTTCTCAGGGAAGATG  
 GAATTTAGTTTTAAGGAAAGAGGAGAACCTCATACTCACAATGAATAGTGATTATGAAATACAGT  
 GTCTCTGAATTAAGCTATGTCTCTCTTCTTAGTTTAGAGGCTCTGTACTTTTATCCATTGATTTTT  
 AACATGGTTCACCACATGTAAGACTGGTGCCTTAGCATCTATGCCACATGCGTTGATGGAAGGTGATA  
 GCACCCACTCACTTAGATGCTAAAGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAAATGATAGC  
 AAGACACATTGAAGCTCTCTTTATACTCAAAGAGATATCCATTGAAAAGGGATGCTCAGAGGGATT  
 TAAACAGCTCCTTTGGCAGCTGCCTCTCTGAATCCAGCCTGCCATTCATCAAATGGAGCAGGAGAGG  
 TGGGAGGAGCTTCTAAAGAGGTGACTGGTATTTGTAGCATTCCTTGCAAGTTCTCCTTTGCAGAA  
 ACCTGTCTCCACATTCCTAGAGAGGAGCCAAAGTTCTAGTAGTTTCAGTTCTAGGCTTTCCTTCAAGAA  
 CAGTCAGATCACAAGAGTGTCTTTGGAATTAAGGGATATTAATTTTAAAGTGATTTTGGATGGTTAT  
 TGATATCITTTGTAGTAGCTTTTTTTAAAGACTACCAAATGTATGGTGTGCCCTTTTTTTTGTGTTTT  
 TTTTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTCTAGGGACCTAAATACTAGGTACGCTTT  
 GGCACACTGTGCTTCTCACATAACCACCTGTAGCAAGATGGATCATAAATGAGAAGTGTTTGCCTA  
 TTGATTTAAAGCTTATTGGAATCATGTCTTGTCTCTTCGCTCTTTCTTTGCTTTCTTCTCAACTTT  
 TCCTCTAGGCTCTCCTGCCACAATTTGCTGCTTACTGCTGGTGTAAATTTTGTGGGATGAATT  
 CTTATCAGGACAAACCTCTCAGAACTGTAATAATGAAGATAATAATATCTTTATCTTTATCCCTTT  
 CAAAGAAATACCTTTTGTGTCAATGCCCTTTTGTGAGCCCTTAAATACCACCTCCTCATGTGTAA  
 ATTGACACAATCACTAATCTGGTAATTTAAACAATTGAGATAGCAAAAGTGTTTAAACAGACTAGGATA  
 ATTTTTTTTTCATATTTGCCAAATTTTTGTAAACCCCTGTCTTGTCAAATAAGTGATAAATATTGTAT  
 TATTAATTTTATTTTACTTTCTATACCATTTCAAAACACATTACACTAAGGGGGAACCAAGACTAGTT  
 TCTTCAGGGCAGTGGAGCTAGTAGTTTGTAAACGTTTTCTATGACGCATAAGCTAGCATGCCATGTG  
 ATTTATTTCTCTGATGAATTTGTCACTGGATCAGCAGCTGTGGAATAAAGCTGTGTGAGCCCTCTGCT  
 GGCCACAGTGGAGGAAGTAGCACAATAGGATACAGTTGTATGTAGTCAATTGGCAACAATTCATACAT  
 ATTTTACTACCAAGAGAGGTATAGTATGGAAGTCCAAATGACTTCTGTATGGATGTGATTAACAGCT  
 GACTGGTGTGAGACTTGAGGTTTCACTAGTCTCTTCAAACATATAGTTTGCCTAGATCTCTCTGGA  
 AACTGACTTTTGTCAAATAAATAGCAGATTGTAGTGTCAAAAAAA

**FIGURE 56**

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL  
 YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMILLVDQ  
 IGNSHVHSTDDPEAARSSNSKITTTTLGLVVHAAADGVALGAAASTQTSVQLIVFVAIMLHK  
 APAAFGLVSFLMHAGLERNRIRKHLVLFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML  
 FSAGTFLYVATVHVLPVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPILISVGHQH

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 37-56, 106-122, 211-230, 240-260, 288-304



**FIGURE 57**

GCTCGAGGCCGGCGCGCGGGAGAGCGACCGGGCGGCCTCGTAGCGGGGCCCGGATCCC  
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTCAGCGCTGATTTTGAGATGATGGGCTTGG  
 GAAACGGGCGTCGCAGCATGAAGTCGCCGCCCTCGTGCTGGCGCCCTGGTGGCTGCATC  
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCCGGAGCGTGGACCTCCAGACACGGAT  
 CATGGAGCTGGAAGGCAGGCTCCGAGGGCGGCTGCAGAGAGAGGCGCGGTGGAGCTGAAGA  
 AGAACGAGTTCAGGGAGAGCTGGAGAAGCAGCGGAGCAGCTTGACAAAATCCAGTCCAGC  
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTTGGTGAA  
 TAACATCACACAGGTGAGAGGCTCATCCGAGTGCTGCAAGACCAAGTTAAAGACCCCTGCAGA  
 GGAATTACGGCAGGCTGCAGCAGGATGTCTCCAGTTTCAGAAGAACCAGACCAACCTGGAG  
 AGGAAGTTCTCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG  
 TGAGGAGCGAATAGAAGAGGTACCAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA  
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG  
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAGGGAACGTGCTTGGTAACAGCAA  
 GTCCCAGACACCAGCCCCAGTTCCGAAGTGGTTTTGGATTCAAAGAGACAAGTTGAGAAAAG  
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCGCAGGAG  
 CCAGGCCGGGAGCAGGTGGTGAAGACAGACCTGTAGGTGGAAGAGGCTTCGGGGGAGCCGG  
 AGAACTGGGCCAGACCCACAGGTGCAGGCTGCCCTGTCTAGTGAGCCAGGAAAATCCAGAGA  
 TGGAGGGCCCTGAGCGAGACCAGTTGTCTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT  
 GCCGGGAAGGGAGAAAACAGCAGAACTGAGAGGAGAAGATGACTACAACATGGATGAAAA  
 TGAAGCAGAACTCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAAACATAGATG  
 TTTTAAATGTTGAAGATCAGAAAAGAGACACCATAAATTTACTTGATCAGCGTGAAAAGCGG  
 AATCATACACTCTGAATTGAACTGGAATCACATATTTACAACAGGGCCGAAGAGATGACTA  
 TAAATGTTTCATGAGGGACTGAATACTGAAAACGTGAAATGTACTAAATAAAATGTACATCTGA

**FIGURE 58**

MMGLGNRRSMKSPPLVLAALVACIIVLGFNYWIASRSVDLQTRIMELEGRVRRAAAERGA  
 VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL  
 KTLQRNYGRQLQQDVLQFQKNQTNLERKFSYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA  
 SRDLSENNDRQQQLQALSEPQPRQAAGLPHTVEVPQKGKGNVLGNSKSQTPAPSSEVVLDSKR  
 QVEKEETNEIQVVNEEPQRDRLPQEFGREQVVEDRPVGGRGFGGAGELGQTPQVQAALSVSQ  
 ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQKLRGEDDYNMDENEAESETDKQAALAGND  
 RNIDVFNVEDQKRDITINLLDQREKRNHTL

**Signal peptide:**

amino acids 1-29

**FIGURE 59**

GGATGCAGAAAGCCTCAGTGTGTCTCTTCTGGCCTGGGTCTGCTTCTCTTCTACGCTGGCAATTGCCCTCTTCA  
 CCAGTGTGCTTCTGCTCACCCGCTTTGGAGCTCACCAACCATAGCAGCTGCCAAGAGCCCCCAGGCCCCCTGGGTGCC  
 TGCCATGGGGAGGCCAAGGAAACCTGGGGCCTGCTGGATGGCTTCCGATTTTTCGGGGTGTGTGTTGGTGTGA  
 TAGATGCTCTGGGATTTGACTTGGCCAGGCCAGCATTCACAGTGCCTAGAGAGCCTCTGCTCTCCCTACCCCT  
 TCTTGGGCAAACTAAGCTCCTTGCAGAGGATCCTGGAGATTACAGCCCCACCATGCCGGCTCTACCGATCTCAGG  
 TTGACCCCTCTACCAACCACTACGAGCGCCTCAGGCCCTCACCACTGGCTCAGTGCCTACCTTTATTTGATGCTG  
 GTAGTAACCTTCGCCAGCCAGGCCATAGTGAAGACAATCTATTAGCAGCTCCACCTGCAGGAAGCGCTGTAG  
 TCTTCTAGGGAGATGATACCTGTGAAGACCTTTTCCCTGGTGTCTTCTCCAAAGCTTCTTCTTCCCATTCTTCA  
 ATGTCCAGAGACTTAGACAGCTGGACAATGGCATCTGCGAACCTCTACCCCACTGCAGCAGTGGTGAATGGG  
 ACGTGCTGATTGCTCACTTCTGGGTGTGGACACTGTGGCCACAAGCATGGCCCTCACCACTGAAATGGGCA  
 AGAACTTAGCCAGATGGACCACTGATCCAGGACTTGTGGAGCTCTGGAGATGACACACTGCTGGTAGTGG  
 CTGGGGACCATGGATGACCACAATGGAGCACTGGAGGGGACAGTGAAGCTGGAGGTCTCAGCTGCTCTCTTTC  
 TGTATAGCCCCACAGCAGTCTTCCCAGCACCCACAGGAGGCCAGAGTGATTCTCCTCAAGTTAGCCTTTGTG  
 CCAGCTGGCCCTGCTGCTGGGCTGCCATCCCATTGGGAATATCGGGGAAGTGTAGTGGCTGAGCTATTCTCAG  
 GGGGTGAGGACTCCAGCCCCACTCCTCTGCTTTAGCCCCAAGCCTCAGCTCTCCATCTCAATGCTCAGCAGGTGT  
 CCCGATTCTTATACCTACTCAGCTGCTACTCAGGACCTTCAAGCTAAGGAGCTTATCAGCTGCAGAACCTCT  
 TCTCCAAAGGCTCTGCTGACTACCACTGGCTTCTCCAGAGCCCAAGGGGCTGAGGCGACACTGCCGACTGTGA  
 TTGCTGAGCTGCAGCACTTCTGCGGGAGCTCGGGCATGTGCATCAGCTTGGGCTCGTTTCTCTCTGGTGC  
 GCATGGCGGGGGTACTGCTCTTGGCTGCTTCTGCTTATCTGCTGCTGCACTGCTAGGCGAATATCCC  
 CAGGCTTTCATTCTTGCGCTCTACTCCTGACACCTGTGGCTGGGGCCTGGTGGGGCCTAGGCTATCTCTGAC  
 TCTTGGGAATTTAGCTGAACTAGATCTAGTGTCTTACGGGCTCTGCGTGCATCTGAGCTCAATTCCTCCTT  
 TTCTGCGGAAGCCTGGGCTGGCTGGGGTCCAAAGGCCCTGCCAACCTGTGTTCCATCCCTGGGCCCCCTC  
 GTTATCTCTGCTGTTTCCGCTTGGCTGTCTTCTCTGATAGTTTTGTTGTAGCTGAGGCGAGGGCCACCCCT  
 TCCCTTTGGGCTCATTCATCCTCTGCTGTGTTGTCAGCTTCACTGGGAGGGCAGCTGCTTCCACTAAGCTAC  
 TCACAAATGCCCCCTGTGGCACTTCAGCCACAACAAACCCCCACGGCAATGGTGATATGCCCTGAGGCTTG  
 GAATGGGTGCTTTTATGATCAAGGCTAGCTGGGCTTTTTCATCGTGTGCCCTGAAGAGACACTGTGTTGCCACT  
 CCTCTCCCTGGCTGAGTCTCTGGCATCCATGGTGGGTGGTCGAGCCAGAATTTATGGTATGGAGCTTGTGTG  
 CGGGCTGGTGGCCCTGTTAGTGCCGTGGCGCTTGTGGCTCGGCCCTATGGTAATCTCAAGAGCCCCGAGCCG  
 CCATGCTCTTTGTGGCTGGGAGTGCCCCCTAATGGCATTGGGTACTGCTGCCTACTGGGCATTGGCGTGGGG  
 CAGATGAGGCTCCCCCGCTCTCCGGTCTGGTCTCTGGGCACTCATGGTGGTGGCTCGGGCTGTAGCAGGGC  
 TGGCTGCTTCAGGGCTCGGCTGCTGCTTGAAGCCTGTGACAGTGTGGTGAAGGCTGGGGCAGGCGCTCAA  
 GGACAGGACTGTCTCACTCCCTTCTCAGGCCCCCCACTTCTCAAGCTGACTTGGATTATGTGTTCCCTCAA  
 TCTACCGACATGTCAGGAGGAGTTCCGGGGCCGGTTAGAGAGGACCAAACTCAGGGTCCCCCTGACTGTGGCTG  
 CTTATCAGTTGGGAGTGTCTACTCAGCTGCTATGGTCACAGCCCTCACCOCTGTTGGCTTCCCACTTCTGCTG  
 TGCATGCGGAGCGCATCAGCTTGTGTTCTGCTCTGTTTCTGACAGCTTCCCTCTCTACATCTGCTGTGCTG  
 TGGGATACCCCTCACCACCCCTGGTCTTTTACTGTGCCATGGCAGGCACTCGGCTTGGGCCCTCATGGCCA  
 CACAGACCTTCTACTCCACAGGCCACAGCCTGTCTTCCAGGCATCCATTGGCATGCAGCCTCTGTTGGGATTC  
 CAGAGGCTCATGGCTCCGTACTTGGCTGCCCTTGTGCTAGTGGAGCCAAACCTTTGGCTCCCCACTCTCTCT  
 TTGCAAGTGGTTGCCACTGCTCCTGCTGTGGCTTCTGTGTGAGAGTCAAGGGCTGCGGAAGAGACAGCAGC  
 CCCCAGGATGAAGCTGATGCCAGAGTACAGCCGAGGAGGAAGAGGACCATGATGGAGATCGGGCTCGGG  
 ATGGCCTCAGCACTTCTATGCAGCACTGCTGCAGCTGGGCCCTCAAGTACCTCTTTATCCTTGGTATTCAGATT  
 CTGGCCTGTGCTTGGCAGCCTCATCTTGCAGGCACTCATGGTCTGGAAAGTGTGTTGCCCTAAGTTCAAT  
 TTGAGGCTGTGGGCTTCAATGTGAGCAGCGTGGGACTTCTCCTGGGCATAGCTTTGGTGTATGAGAGTGGATGGTG  
 CTGTGAGCTTGTGAGCAGCTATTTTGGCCAGCAGAGT**AGC**CTAGTCTGTGATTACTGGCACTTGGCT  
 ACAGAGAGCTGTGGAGACAGTGTAGCTGGCTGTACAGTACTGGATGATCTGCAAGACAGGCTCAGCCATAC  
 TCTTACTACTCATGCAGCCAGGGGCCGTGACATCTAGGACTTCAATTTCTATTAATTCAGGACACAGTGGAGTA  
 TGATCCCTAACTCCTGATTTGGATGCATCTCAGGACAGGGGGGGCTTCCGAAGTGGAAATAAATAGGCCGG  
 CGGTGGTCACTTCACTTAACTCCAGCACTTTGGGACGAGAGGTGGGAGATGCTTGGTCCAGAGGTTCA  
 AGACCAGCCTGTGGAACTAACAGACCCCTCTCTACTATTTAAAAAAGTGAATAAATGATAATAT

**FIGURE 60**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809

<subunit 1 of 1, 1089 aa, 1 stop

<MW: 118699, pI: 8.49, NX(S/T): 2

MQKASVLLFLAWVCFLYAGIALFTSGFLLTRLELTNHSSCQEPPGPGSIPWGSQGKPGACW  
 MASRFSRVVLIDALRFDAQPHSHVPREPPVSLPFLGKLSSLRILEIQPHHARLYRSQ  
 VDPPTTMMQRLKALTGTSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRRVVFMGDDTWKDLF  
 PGAFSKAFFPFSFNVRLDLDVNGILEHLYPTMDSGEWDVLIHFLGVDHCGHKHGPHPPEM  
 AKKLSQMDQVIQGLVERLENDTLLVVAGDHGMTNGDHGGDSELEVSAALFLYSPTAVFPST  
 PPEEPEVIPQVSLVPTLALLGLPIPFNGIGEVMAELFSGGEDSQPHSSALAQASALHNAQ  
 QVSRFLHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAETLPTVIAELQQFLRG  
 ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAI SPGFPCPLLLTPVAWGLVGAIA  
 YAGLLGTIELKLDLVLLGAVAAVSSFLPFLWKAWAGWGSKRPLATLFPPIPGPVLLLLLRLA  
 VVFSDSFVVAERATPFLGGSFILLVVLHWEGQLLPKLLTMPRLGTSATTNPPRHNGAY  
 ALRLGIGLLLCITRLAGLFHRCPEETPVCHSSPWLSPLASMVGGRAKNLWYGACVAALVALLA  
 AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAAYWALASGADEAPPRLRVLVSGASMLP  
 RAVAGLAASGLALLLWKPVTVLVKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE  
 EFRGRLERTKSQGPI TVAAYQLGSVYSAMVTALTLLAFPLLLHAERISLVFLLFLQSFL  
 LLHLLAAGIPVTTTGPFTVPWQAVSAWALMATQTFYSTGHQPVFPAIHWAAAFVGFPEGHGS  
 CTWLPALLVGANTFASHLLFAVGCPLLLLPFLCESQGLRKRQPPGNEADARVRPEEEEEEP  
 LMEMRLRDAPQH FYAALLQLGLKYLFI LGIQILACALAASILRRHLMVWKVFAPKFI FEAVG  
 FIVSSVGLLLGIALVMRVDGAVSSWFRQLFLAQQR

**Important features:****Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,  
 1016-1034, 1052-1070

**Leucine zipper pattern.**

amino acids 843-864

**N-glycosylation sites.**

amino acids 37-40, 268-271

**FIGURE 61**

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCGCCTTGGGGACGGGCAGTTCCCTGT  
 GTCTCTGGTGGTTTGCCTAAACCTGCAAACATCACCTTCTTATCCATCAACATGAAGA**AATGT**  
 CCTACAATGGACTCCACCAGAGGGTCTTCAAGGAGTTAAAGTTACTTACACTGTGCAGTATT  
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTTCTGTTGT  
 CCTGACAGCTCCAGAGAAGTGGAGAGAAAATCCAGAAGACCTTCTGTGTTCCATGCAACAAA  
 TATACTCCAATCTGAAGTATAACGTGTCTGTGTTGAATACTAAATCAAACAGAACGTGGTCC  
 CAGTGTGTGACCAACCACACGCTGGTGTCTACCTGGCTGGAGCCGAACACTCTTTACTGCGT  
 ACACGTGGAGTCCTTCGTCCCAGGGCCCCCTCGCCGTGTCTAGCCTTCTGAGAAGCAGTGTG  
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAAATCATCTTCTGGTATGTTTTG  
 CCCATATCTATTACCGTGTCTTTTTTCTGTGATGGGCTATTCCATCTACCGATATATCCA  
 CGTTGGCAAAGAGAAAACCCAGCAAATTTGATTTTGATTTATGAAATGAATTTGACAAAA  
 GATTCCTTTGTGCTGCTGAAAAAATCGTGATTAACCTTTATCACCTCAATATCTCGGATGAT  
 TCTAAAAATTTCTCATCAGGATATGAGTTTACTGGGAAAAGCAGTGATGTATCCAGCCTTAA  
 TGATCCTCAGCCAGCGGGAACTGAGGCCCCCTCAGGAGGAAGAGGAGGTGAAACATTTAG  
 GGTATGCTTCGCATTTGATGGAAATTTTTTGTGACTCTGAAGAAAACACGGAAGTACTTCT  
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCGGATAAAAACAGTCATTGAATATGA  
 ATATGATGTGAGAACCACACTGACATTTGTGCGGGGCTGAAGAGCAGGAGCTCAGTTTGCAGG  
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTTGGGCCCG  
 CAAACGTTACAGTACTCATAACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA  
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCTGGTCGACTGGGATCCCC  
 AAACCTGGCAGGCTGTGTATTCCTTCGCTGTTCAGCTTCGACAGGATTACAGAGGCTGCGAG  
 CCTTCTGAGGGGGATGGGCTCGGAGAGGAGGCTCTTCTATCTAGACTCTATGAGGAGCCGGC  
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCATGGAGGAATGGGGGT  
 TATATGTGCAGATGGAAAC**TGA**TGCCAACACTTCCTTTTGCTTTTGTTTCTGTGCAAAC  
 AAGTGAGTCACCCCTTTGATCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTTCCAGT  
 TTGTGAGTGTCTGTGAGAATTACTTATTTCTTTCTCTATTCTCATAGCACGTGTGTGATTG  
 GTTATGCATGTAGGTCTCTTAACAATGATGGTGGGCCCTCGGAGTCCAGGGGCTGGCCGGT  
 TGTTCTATGCAGAGAAAGCAGTCAATAAATGTTTGCCAGACTGGGTGCAGAATTTATTCAGG  
 TGGGTGT

**FIGURE 62**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815

<subunit 1 of 1, 442 aa, 1 stop

<MW: 49932, pI: 4.55, NX(S/T): 5

MSYNGLHQRVFKELKLLTLCSSQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ  
QIYSNLKYNVSVLNTKSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVGPPIRRAPSEKQ  
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNFED  
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEEVKH  
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPDPKTVIEYEDVVRTDICAGPEEQELSL  
QEEVSTQGTLLSQAALAVLGPQTLQYSYTPQLQDLPLAQEHTDSEEGPEEEPSTTLVDWD  
PQTGRLCIPSLSSFQDSEGCEPSEGDLGEEGLLSRLYEPPAPDRPPGENETYLMQFMEEW  
GLYVQMEN

**Important features:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 140-163

**N-glycosylation sites.**

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

**FIGURE 63**

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGTCTCTGCGGGGAGACGCCAGCCTGCG  
TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGGACGTCTCTGCTGACTGTGGCCACCGCCCT  
GATGCTGCCCCGTGAAGCCCCCGCAGGCTCCTGGGGGGCCAGATCATCGGGGGCCACGAGG  
TGACCCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGGCCAACATCACTGCGGA  
GGCTTCTCTGCTGCGAGCCCGCTGGGTGGTCTCGGCCGCCCACTGCTTCAGCCACAGAGACCT  
CCGCACTGGCCTGGTGGTGTCTGGGCGCCACGTCCTGAGTACTGCGGAGCCCACCCAGCAGG  
TGTTTGGCATCGATGCTCTCACCACGCACCCGACTACCACCCCATGACCCACGCCAACGAC  
ATCTGCCTGCTGCGGCTGAACGGCTCTGCTGTCTGGGCCCTGCAGTGGGGCTGCTGAGGCT  
GCCAGGGAGAAGGGCCAGGCCCCCCACAGCGGGGACACGGTGCCGGGTGGCTGGCTGGGGCT  
TCGTGTCTGACTTTGAGGAGCTGCCGCTGGACTGATGGAGGCCAAGGTCCGAGTGTCTGGAC  
CCGGACGTCTGCAACAGCTCCTGGAAGGGCCACCTGACACTTACCATGCTCTGCACCCGCAG  
TGGGGACAGCCACAGACGGGGCTTCTGCTCGGCCGACTCCGGAGGGCCCTGGTGTGCAGGA  
ACCGGGCTCACGGCCTCGTTTCCTTCTCGGGCCTCTGGTGCGCGACCCCAAGACCCCGAC  
GTGTACACGCAGGTGTCCGCCTTTGTGGCCTGGATCTGGGACGTGGTTTCGGCGGAGCAGTCC  
CCAGCCCGGCCCTGCCTGGGACCACCAGGCCCCAGGAGAAGCCGCGCTTGAGCCACAACCT  
TGCGCATGCAAAATGAGATGGCCGCTCCAGGCCCTGGAATGTTCCGTGGCTGGGCCCCACGGG  
AAGCCTGATGTTTCAAGGTTGGGGTGGGACGGGACGCGGTGGGGCACACCCATTCCACATGCA  
AAGGGCAGAAGCAAACCCAGTAAATGTTAACTGACAAAAAAGAAA

**FIGURE 64**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVATALMLFPVKPPAGSWGAIIGGHEVTPHSRPYMASVRFGGQHHCGGF
LLRARWVVSAAHCFSHRDLRTGLVVLGAHVLSTAEP TQQVFGIDALTTHPDYHPMTHANDIC
LLRLNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEAKVRVLDPD
VCNSSWKGHLLTLMCLTRSGDSHRRGFCSADSGGPLVCRNRAHGLVSFSGLWC G DPKTPDVY
TQVSAFVAWIWDVVRSSPQPGPLPGTTRPPGEAA
```

**Signal peptide:**

amino acids 1-30



**FIGURE 65**

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCGCCGACTCCGAGACGCTGACGCCTGA  
 CGCCTGTCCCCGGCCCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTGCGGCGTGGGCACGGTAG  
 CAGGCGCCGCGTGTCTCAAGGACTATGTACCCGGTGGGGCTTGCCCCAGCAAGGCCACC  
 ATCCCTGGGAAGACGGTCATCGTGACGGGCGCCAACACAGGCATCGGGAAGCAGACCGCCTT  
 GGAATGGCCAGGAGAGGAGGCAACATCATCCTGGCCTGCCGAGACATGGAGAAGTGTGAGG  
 CGGCAGCAAAGGACATCCGCGGGGAGACCCTCAATCACCATGTCAACGCCCGGCACCTGGAC  
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTTGACAGCAAAGATCATTGAAGAGGAGGAGCGAGT  
 GGACATTCTAATCAACAACGCGGGTGTGATGCGGTGCCCCCACTGGACCACCGAGGACGGCT  
 TCGAGATGCAGTTTGGCGTTAACCACCTGGGTCACTTCTCTTGACAAACTTGCTGCTGGAC  
 AAGCTGAAAGCCTCAGCCCCCTTCGCGGATCATCAACCTCTCGTCCCTGGCCCATTGTTGCTGG  
 GCACATAGACTTTGACGACTTGAAGTGGCAGACGAGGAAGTATAACACCAAAGCCGCCCTACT  
 GCCAGAGCAAAGCTCGCCATCGTCTCTTCACCAAGGAGCTGAGCCGGCGGCTGCAAGGCTCT  
 GGTGTGACTGTCAACGCCCTGCACCCCGGCGTGGCCAGGACAGAGCTGGGCAGACACACGGG  
 CATCCATGGCTCCACCTTCTCCAGCACCACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA  
 GCCCGAGCTGGCCGCCAGCCAGCACATACCTGGCCGTGGCGGAGGAAGTGGCGGATGTTT  
 TCCGGAAGTACTTCGATGGACTCAAACAGAAGGCCCGGCCCGGAGGCTGAGGATGAGGA  
 GGTGGCCCGGAGGCTTTGGGCTGAAAGTGCCCGCTGGTGGGCTTAGAGGCTCCCTCTGTGA  
 GGGAGCAGCCCCCTCCCAGAT**TAA**ACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCCTCCAG  
 ACCGAGGACAGCTGTCCGCCATGCCCGCAGCTTCCTGGCACTACCTGAGCCGGGAGACCCAG  
 GACTGGCGGCCGCCATGCCCGCAGTAGGTTCTAGGGGGCGGTGCTGGCCGAGTGACTGGC  
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTTCCGTCTGCTCTGCTGCCAGCAGGGGAG  
 AGGGGCCATCTGATGCTTCCCTGGGAATCTAAACTGGGAATGGCCGAGGAGGAAGGGGCTC  
 TGTGCACTTGACAGCCACGTGAGGAGGCCAGCGGTGCTGTGCGGGAGGGTTCCAAGGTGC  
 TCCGTGAAGAGCATGGGCAAGTTGTCTGACACTTGGTGGATTCTTGGGTCCCTGTGGGACCT  
 TGTGCATGCATGGTCCCTCTCTGAGCCTTGGTTTCTTCAGCAGTGAGATGCTCAGAATAACTG  
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTGTCTGGCTATGGCATGGCTGTGCCGGG  
 GGTGTTTGTCTGAGGGCTTCTGTGCCAGAGCCAGCCAGAGAGCAGGTGCAGGTGTATCCC  
 GAGTTCAGGCTCTGCACGGCATGGAGTGGGAACCCCAACAGCTGCTGTCTACAGGACCTGGGA  
 TTGCTGGGACTCCCACCTTCTATCAATTCTCATGTTAGTCCAAACTGCAGACTCTCAAC  
 TTGCTCATTT

**FIGURE 66**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842

><subunit 1 of 1, 331 aa, 1 stop

><MW: 35932, pI: 8.45, NX(S/T): 1

MSRYLLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG  
GNIILACRMEKCEAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERV DILINN  
AGVMRCPHWTTEDGFEMQFGVNH LGHFLLTNLLLDK LKASAPSRIINLSSLAHVAGHIDFDD  
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELG RHTGIHG STF  
SSTTLGPIFWLLVKSP ELAAQPSTYLAVAEELADVSGKYFDGLKQKAPAPEAEDEEVARRLW  
AESARLVGLEAPSVREQLPR

**Signal peptide:**

amino acids 1-17

**FIGURE 67**

GAAGTTCGCGAGCGCTGGC**ATG**TGGTCTGGGGCGCGGCTGGCGGCGCTGCTGGCGGTGCTG  
 GCGCTCGGGACAGGAGACCCAGAAAAGGGTGC GGCTCGGGGCGACACGTTCTCGGCGCTGAC  
 CAGCGTGGCGCGCGCCCTGGCGCCCGAGCGCGGCTGCTGGGGCTGCTGAGGCGGTACCTGC  
 GCGGGGAGGAGGCGCGGCTGCGGGACCTGACTAGATTCTACGACAAGGTA CTTTCTTTGCAT  
 GAGGATTCAACAACCCCTGTGGCTAACCCCTCTGCTTGCATTTACTCTCATCAAACGCGCTGCA  
 GTCTGACTGGAGGAATGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG  
 ATGGCTATGAGAAGGTGGAGCAAGACCTTCCAGCCTTTGAGGACCTTGAGGGAGCAGCAAGG  
 GCCCTGATGCGGCTGCAGGACGTGTACATGCTCAATGTGAAAGGCCTGGCCCCGAGGTGCTTT  
 TCAGAGAGTCACTGGCTCTGCCATCACTGACCTGTACAGCCCCAAACGGCTCTTTTCTCTCA  
 CAGGGGATGACTGCTTCCAAGTTGGCAAGGTGGCCTATGACATGGGGGATTATTACCATGCC  
 ATTCCATGGCTGGAGGAGGCTGTAGTCTCTTCCGAGGATCTTACGGAGAGTGGAAGACAGA  
 GGATGAGGCAAGTCTAGAAGATGCCTTGGATCACTTGGCCTTTGCTTATTTCCGGGCAGGAA  
 ATGTTTCGTGTGCCCTCAGCCTCTCTCGGGAGTTTCTTCTCTACAGCCCAGATAATAAGAGG  
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTTGGCAGAGAGCCCCAACACGCTGGTAGC  
 TGAGGCTGTCTACAGAGGCCAATATACCCACCTGCAGACCAGAGACACCTACGAGGGGC  
 TATGTACAGCCCTGGGTTCCAGCCCACTCTCTACAGATCCCTAGCCTCTACTGTTCCAT  
 GAGACCAATTCGAAGCCTACCTGTCTGCCAGCCCATCCGGAAGGAGGTATCCACCTGGA  
 GCCCTACATTGCTCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAAATTAGAGAAC  
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGA  
 TACCGCATCAGCAAAAGTGCTGGCTGAAGGACACTGTTGACCCAAAAGTGGTGACCCCTCAA  
 CCACGCGATTGCTGCCCTCACAGGCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG  
 TGGTGAACATATGGCATCGGAGGACACTATGAGCCTCACTTTGACCATGCTACGTCAACAGC  
 AGCCCCCTCTACAGAATGAAGTCAGGAACCGAGTTGCAACATTTATGATCTATCTGAGCTC  
 GGTGGAAGCTGGAGGAGCCACAGCCTTCATCTATGCCAACCTCAGCGTGCCTGTGGTTAGGA  
 ATGCAGCACTGTTTTGGTGGAACTGCACAGGAGTGGTGAAGGGGACAGTGACACACTTCAT  
 GCTGGCTGTCTGTCTGGTGGGAGATAAGTGGGTGGCCAAAGTGGATACATGAGTATGG  
 ACAGGAATTCGCGAGACCCTGCAGCTCCAGCCCTGAAGACT**GAA**ACTGTTGGCAGAGAGAAGC  
 TGGTGGAGTCTGTGGCTTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGGTAGGAGAGAGAA  
 AGCAGAGCAGCCTCCTGGAAAGAGGCCTTGCTAGCTTTGTCTGTGCCTCGCAAATCAGAGGC  
 AAGGGAGAGGTTGTTACAGGGGACACTGAGAATGTACATTTGATCTGCCCGAGCCAGGAA  
 GTCAGATAGGATGCAAGTACAAAGGAGGGGGAGTGGAGGCCCTGAGAGGGAAGTTTCTGG  
 AGTTCAGATACTCTCTGTTGGGAACAGGACATCTCAACAGTCTCAGGTTGCATCAGTGGGTG  
 TTTTGGCACTTTGAACCTTGACCAAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG  
 GGGCTAGCCTGACTCCAGAACTTTAAGACTTTCTCCCCACTGCCTTCTGCTGCAGCCCAAG  
 CAGGAGATGTCGCCCTCCCAAGCATATCCAGATGAGTGGTACATTATAGGATTTTT  
 TTTAAGTTGAAAACAACCTTTCTTTCTTTTGTATGATGGTTTTTTAACACAGTCATTAAAA  
 ATGTTTATAAATCAAA

**FIGURE 68**

MGPGARLAALLAVLALGTGDPERAAARGDTFSALTSVARALAPERLLGLLRRYLRGEEARL  
 RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRLQSDWRNVVHSLEASENIRALKDGYEKVE  
 QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRTGSAITDLYSPKRLFSLTGDDCFQ  
 VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHLAFAYFRAGNVSCALS  
 LSREFLLYSPDNKRMRNVLYKYLRLAESPNHVVAEVIQRPNI PHLQTRDTYEGLCQTLGS  
 QPTLYQIPSLYCSYETNSNAYLLQPIRKEVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ  
 RSVVASGEKQLQVEYRISKSAWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG  
 GHYEPHFDHATSPSSPLYRMKSGNRVATFMIYLSSEAGGATAFIYANLSVPVVRNAALFWW  
 NLHRSGEGSDTLHAGCPVLVGDKWVANKWIEHYGQEFRPCSSSPED

**Signal peptide:**

amino acids 1-19

**FIGURE 69**

GAGATAGGGAGTCTGGGTTTAAAGTTCCTGCTCCATCTCAGGAGCCCTGCTCCACCCCTAG  
 GAAGCCACCAGACTCCACGGTGTGGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC  
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCGTAACCCGCGCGGGGAG  
 CGCCAGG**ATG**CCGCGCGGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC  
 TGGCTCAAGTTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGGCCCTGGTCCT  
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCCCTGAAAGTGCCCTCC  
 TGGCTCCAGCCATCATCTCATCCTCCTGGGCGTCGTCATGTTATGGTCTCCTTCATTGGT  
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCTCCAAGCATTCATGTACATCCTTGGGAT  
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGGAACCAGACCATTG  
 ACTTCTGAACGACAACATTCGAAGAGGAATTGAGAACTACTATGATGATCTGGACTTCAAA  
 AACATCATGGACTTTGTTTCAGAAAAAGTCAAGTGCTGTGGCGGGGAGGACTACCGAGATTG  
 GAGCAAGAATCAGTACCAGACTGCAGTGCCCTTGACCCCTGGCCTGTGGGGTGCCCTACA  
 CCGTGTGCATCAGGAACGACAGAGAAGTTGTCAACACCATGTGTGGCTACAAAACATATCGAC  
 AAGGAGCGTTTCAGTGTGCAGGATGTCACTACGTGCGGGGCTGCACCAACGCCGTGATCAT  
 CTGGTTTCATGGACAACACACCATCATGGCGTGCATCCTCCTGGGCATCCTGCTTCCCCAGT  
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGGTGGAGGACATCATCATGGAGCAC  
 TCTGTCACTGATGGGCTCCTGGGGCCCGGTGCCAAGCCAGCGTGGAGGCGGCAGGCACGGG  
 ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC  
 TGGGATAGCACCTCTCAGTCAACATCGTGGGGCTGGACAGGGCTGCGGCCCTCTGCCACA  
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCTGTGTGTAGTCCCACGGCCTCTGCCTC  
 CCCAGGGAGCAGAGCCTGGGCCTCCCTTAAGAGCCTTCCCGAGGCAGCTCTGGAATCTGT  
 GCCCACCTGGGGCCTGGGGAACAAGGCCCTCCTTCTCCAGGCCTGGGCTACAGGGGAGGGA  
 GAGCCTGAGGCTCTGCTCAGGGCCCATTTTCATCTCTGGCAGTGCCTTGGCGGTGGTATTCAA  
 GGCAGTTTTGTAGCACCTGTAATTGGGGAGAGGGAGTGTGCCCTCGGGGCAGGAGGGAAGG  
 GCATCTGGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCCAGGTGGC  
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTCTTGAAGGGCGGCTGCTTCTTGAAGCCTA  
 GTTTTTTTTTACGTGATTTTTTGTAAACATTCATTTTTTTGTACAGATAACAGGAGTTTCTGAC  
 TAATCAAAGCTGGTATTTCCCGCATGTCTTATCTTGCCCTTCCCCAACCAAGTTTGTGTTAA  
 TCAAACAATAAAAAACATGTTTTGTTTTGTTTTAAAAA

**FIGURE 70**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYLWLKFSLLIYSTVFWLIGALVLSVGIYAEVERQKYKTLES AFLAP
AIIILILGVVMFMVSFIGVLASLRDNLVLLQAFMYILGICLIMELIGGVVALTFRNQ TIDFL
NDNIRRGIEENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIIYVRGCTNAV IIFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTDGLLGP GAKPSVEAAGTGCCLCYPN
```

**Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 22-42, 57-85, 93-116, 230-257

**FIGURE 71**

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCTGCACTTGCTGCCCTCTGA  
 CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCCTCTCTGTGTTTGTCTGGCAGCCACC  
 TTGATCCAAGCCACCCTCAGTCCCAGTCTCATCCTCGGCCCAAAAGTCATCAAAGA  
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC  
 TCAGTGCCATGCGGGAAAAGCGAGCCGGAGGCATCCCTGTGTGGGCAGCCTGGTGAAACCC  
 GTCCTGAAGCACATCATCTGGCTGAAGGTCATCACAGCTAACATCCTCCAGCTGCAGGTGAA  
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA  
 ACACGCCCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCCAAGCCACCATC  
 CGCATGGACACCAGTGCAAGTGGCCCCACCCGCTGGTCTCAGTGACTGTGCCACCAGCCA  
 TGGGAGCCTGCGCATCCAACCTGCTGTATAAGCTCTCCTTCTGGTGAACGCCTTAGCTAAGC  
 AGGTCATGAACCTCCTAGTGCCATCCCTGCCCAATCTAGTGAAAAACCAGCTGTGTCCCGTG  
 ATCGAGGCTTCCTTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCCATTTT  
 CCTCAGCATTGACCGTCTGGAGTTTGACCTTCTGTATCCTGCCATCAAGGGTGACACCATT  
 AGCTCTACCTGGGGCCCAAGTTGTTGGACTCACAGGAAAGGTGACCAAGTGGTTCAATAAC  
 TCTGCAGCTTCCCTGACAATGCCACCCTGGACAACATCCCCGTTTACGCTCATCGTGAGTCA  
 GGACGTGGTGAAAGCTGCAGTGGCTGCTGTGCTCTCTCCAGAAGAATTATGGTCTGTTGG  
 ACTCTGTGCTTCTGAGAGTGCCCATCGGCTGAAGTCAAGCATCGGGCTGATCAATGAAAAG  
 GCTGCAGATAAGCTGGGATCTACCCAGATCGTGAAGATCCTAACTCAGGACACTCCCGAGTT  
 TTTTATAGACCAAGGCCATGCCAAGGTGGCCCAACTGATCGTGCTGGAAGTGTTTCCCTCCA  
 GTGAAGCCCTCCGCCCTTTGTTACCCCTGGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC  
 ACCAAAGGTGACCAACTTATACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT  
 GAACTCTGGGATTGGCTGGTTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC  
 ACTCCATCTGTCTGCCGAACAGAATGGCAAATTAAGATCTGGGGTCCCAGTGTCATTGGTG  
 AAGGCCTTGGGATTCGAGGCAGCTGAGTCTCTACTGACCAAGGATGCCCTTGTGCTTACTCC  
 AGCCTCCTTGTGAAACCAGCTCTCCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG  
 GGAAGGCTGGGTCCCAGCTGGGAGTATGGGTGTGAGCTCTATAGACCATCCCTCTCTGCAAT  
 CAATAAACAATGGCTGTGAAAA

**FIGURE 72**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881  
><subunit 1 of 1, 484 aa, 1 stop  
><MW: 52468, pI: 7.14, NX(S/T): 3  
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM  
REKPAGGI PVLGSLVNTVLKHIIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL  
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN  
LLVPSL PNLVKNQLCPVIEASFNGMYADLLQLVKVPI SLSIDRLEFDLLYP AIKGDTIQLYL  
GAKLLDSQ GKVTKWFNN SAASLT MPTLDNIPFSLIVSQDVVKA AAVLSPEEFMVLLDSVL  
PESAHRLKSSIGLINEKAADKL GSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSSEAL  
RPLFTL GIEASSEAQFYTKGDQLILNLN NISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL  
LPNQNGKLRSGVPVSLVKALGFEEAESSLT KDALVLT PASLWKPPSSPVSQ

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 48-51, 264-267, 401-404

**Glycosaminoglycan attachment site.**

amino acids 412-415

**LBP / BPI / CETP family proteins.**

amino acids 407-457



**FIGURE 73**

GAGCGAACATGGCGAGCGGTTGGCGGTTTTGGTGTGTCTCTGTGACCATGGTGGTGGCGCTG  
 CTCATCGTTTTGCGACGTTCCCTCAGCCTCTGCCAAGAAAGAAGGAGATGGTGGTATCTGA  
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAGACCTGTAATAAGAATGAATGGAGACA  
 AGTTCGCTCGCCTTGTGAAAGCCCAACCGAGAATTACTCCGTATCGTCATGTTCACTGCT  
 CTCCAACATGCATAGACAGTGTGTCGTTTGCAAGCAAGCTGATGAAGAATCCAGATCCTGGC  
 AAACCTCCTGGCGATACTCCAGTGCATTCCCAACAGGATATTTTTGGCATGGTGGATTTTG  
 ATGAAGGCCTCTGATGTATTTAGATGCTAAACATGAATTCAGCTCCAACCTTTCATCAACTGT  
 CCTGCAAAAGGGAACCAACCGGGTGATACATATGAGTTACAGGTGCGGGTTTTTCTCAGC  
 TGAGCAGATTGCCCGGTGGATCGCCGACAGAATCATGTCAATATTAGAGTGATTAGACCCC  
 CAAATTATGCTGGTCCCTTTATGTTGGGATTGCTTTTGGCTGTTATGGTGGACTTGTGTAT  
 CTTCGAAGAAGTAATATGGAATTTCTCTTTAAATAAAGCTGATGGGCTTTTGACGCTTTGTG  
 TTTTGTGCTTGCTATGACATCTGGTCAAAATGTGGAACCATATAAGAGGACCACCATATGCC  
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAAGCCAGTTTGTA  
 GCTGAAACACACATTGTTCTTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCCTTTATG  
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGTGGCTGGTATTG  
 GACTTGTGTATTTATTTCTCAGTTGGATGCTCTCTATTTTTAGATCTAAATATCATGGCTAC  
 CCATACAGCTTTCTGATGAGTTAAAAAGGTCCCAGAGATATATAGACACTGGAGTACTGGAA  
 ATTGAAAAACGAAATCGTGTGTGTTTGAAGAAGAAGATGCAACTTGTATATTTGTATTAC  
 CTCTTTTTTTCAAGTGATTTAAATAGTTAATCATTTAACCAAGAAGATGTGTAGTGCCTTA  
 ACAAGCAATCCTCTGTCAAAATCTGAGGTATTTGAAATAATTATCCTCTTAACCTTCTCTT  
 CCCAGTGAACCTTTATGGAACATTTAATTTAGTACAATTAAGTATATTTAAAAAATTGTAAA  
 CTACTACTTTGTTTTAGTTAGAACAAGCTCAAACTACTTTAGTTAACTTTGGTCACTGTAT  
 TTTATATTGCCTTATCCAAGATGGGGAAGTAAGTCTGACCAGGTGTTCCACATATGCC  
 TGTTACAGATAACTACATTAGGAATTCATTCTTAGCTTCTTCACTTTGTGTGGATGTGTAT  
 ACTTTACGCATCTTTCCCTTTTGGAGTAGAGAAATATGTGTGTCACTGTGGTCTTCTGAAATG  
 GAACACCATTCTTTCAGAGCACACGCTAGCCCTCAGCAAGACAGTTGTTTCTCCTCCTCCTT  
 GCATATTTCCCTACTGCGCTCCAGCCTGAGTGATAGAGTGAGACTCTGTCTCAAAAAAAGTA  
 TCTCTAAATACAGGATTATAATTTCTGCTTGAGTATGGTGTTAACTACCTTGTATTAGAAA  
 GATTTTCAGATTCACTCCATCTCCTTAGTTTTCTTTTAAAGGTGACCATCTGTGATAAAAAA  
 TAGCTTAGTGCTAAAAATCAGTGTAACTTATACATGGCCTAAAAATGTTTCTACAAATTAGAGT  
 TTGTCACCTTATTCACATTTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG  
 CCAGGCGCAGTGACTTACGCTGTAACTCTCAGCACTTTGGGAGGCCAAGCAGGCAGATCAC  
 GAGGTGAGGAGTTCGAGACCATCCTGGCCAACATGGTGAAACCCCGTCTCTACTAAAAATAT  
 AAAAATTAGCTGGTGTGGTGGCAGAGCCTGTAATCCAGCTACACAGGAGCTGAGGCAC  
 GAGAACTACTTGAACTCAGGAGATGGAGGTTTTAGTGAGCCGAGATCAGCCCATGCACTCC  
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAAAA

**FIGURE 74**

MAARWRFWCVSVTMVVALLIVCDVPSASAQRKKEMVLSEKVSQLMWNTNKRVPVIRMNGDKFR  
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFAMVDFDEG  
SDVFQMLNMNSAPTFINFFAKGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY  
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFALCFVLAMTSGQMWNHIRGPPYAHKN  
PHTGHVNYIHGSSQAQFVAETHIVLLFNNGVTLGMVLLCEAATSDMDIGKRKIMCVAGIGLV  
VLFFSWMLSIFRSKYHGYPYSFLMS

**Signal peptide:**

amino acids 1-29

**Transmembrane domains:**

amino acids 183-205, 217-237, 217-287, 301-321

**FIGURE 75**

**FIGURE 76**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885  
 <subunit 1 of 1, 536 aa, 1 stop  
 <MW: 61450, pI: 9.17, NX(S/T): 7  
 MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVSDSFDGRLTFHPGSQVVKLPFINF  
 MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ  
 KFGKLDYTSGHHSISNRVEAWTRDVAFLLRQEGRPMVNLIRNRTKVRVMERDQNTDKAVNW  
 LRKEAINYTEPFVIYLG LNLPHYPSPSSGENFGSSSTFHTSLYWLEKVS HDAIKI PKWSPLS  
 EMHPVDYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIIY  
 SSDHGELAMEHRQFYKMSMYEASAHVPLLMMPGPGIKAGLQVSNVSLVDIYPTMLDIAGIPL  
 PQNLSGSYLLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS  
 ILPQLFDLSSDPDEL TNVAVKFP EITYSLDQKLHSI INYPKVSASVHQYNKEQFIKWKQSIG  
 QNYSNVIANLRWHQDWQKEPRKYENAI DQWLKTHMNPRAV

**Important features:****Signal peptide:**

amino acids 1-15

**N-glycosylation sites.**

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,  
 498-501

**Sulfatases proteins:**

amino acids 286-315, 359-369, 78-97

**FIGURE 77**

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG  
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATG  
 GCCTCTCTTGGCCTCCAACCTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACT  
 GGTGGCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGCGTGCCAGCATTGTGACAG  
 CAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG  
 TGTGACATCTATAGCACCTTCTGGGCCTGCCGCTGACATCCAGGCTGCCAGGCCATGAT  
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCA  
 CAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTC  
 ATCCTTGGAGGCCCTCCTGGGATTCACTTCTGTTGCCTGGAATCTTCATGGGATCCTACGGGA  
 CTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGG  
 GCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCC  
 CAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTC  
 TCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT  
 ATGTGTGAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG  
 CACCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGTGCTGCTGAGG  
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGCAGAAATGGGGGCTAGTGTAACAGCATG  
 CAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCTCACCTTGCTGCTC  
 CCTGCCCCTAAGTCCCCAACCTCAACTTGAACCCCATTCCTTAAGCCAGGACTCAGAGG  
 ATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAATCACATCCCACTG  
 ACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGG  
 GGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCC  
 TCCAAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTTATGACTCCACAGTGTCC  
 AGACTAATTTGTGCTGAAGTGAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG  
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

**FIGURE 78**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSGKLWMECATHSTGIT
QCDIYSTLLGLPADIQAAQAMMVTSSAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGLLGFIPIVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLSLIAGIILCFSCS
SQRNRSNYDAYQAQPLATRSSPRGQPFPKVKSEFNSSYSLTGYV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 82-102, 117-140, 163-182

**N-glycosylation site.**

amino acids 190-193

**PMP-22 / EMP / MP20 family proteins.**

amino acids 46-59

**FIGURE 79**

GCAC T GCT GCT GTCC ATCAGCTGCTCTGAAGCTCC**ATG**GTGCC CAGAATCTTCGCTCCTGC  
TTATGTGT CAGTCTGTCTCCTCCTCTGTGTCCAAGGGAAGTCATCGCTCCCGCTGGCTCAG  
AACCATGGCTGTGCCAGCCGGCACCCAGGTGTGGAGACAAGATCTACAACCCCTTGGAGCAG  
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCCAATGTGGTCCCCCTGCAC  
CTTCTGGCCCTGCTTTGAGCTCTGCTGTCTTGATTCCCTTGGCCTCACAACGATTTTGTTG  
TGAAGCTGAAGGTT CAGG GTGAATTCC CAGTGCCACTCATCTCCATCTCCAGTAAATGT  
GAAAGCAGAAGACGTTTTCCCT**TG**AGAAGACATAGAAAGAAAATCAACTTTCAC TAAGGCATC  
TCAGAAACATAGGCTAAGGTAATATGTGTACCAGTAGAGAAGCCTGAGGAATTTACAAAATG  
ATGCAGCTCCAAGCCATGTGTATGGCCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT  
AGATTATCAGGAAATAAAATAAAAGTGGTTTTTCCAATGTACACACCTGTAAAA

**FIGURE 80**

MVPRIFAPAYVSVCLLLCPREVIAPAGSEFWLCQPAPRCGDKIYNPLEQCCYNDAIVSLSE  
TRQCGFPCTFWPCFELCCLDSFGLTNDVFVKLVQGVNSQCHSSPISSKCESRRRFP

**Signal peptide:**

amino acids 1-25

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**FIGURE 81**

CTCCACTGCAACCACCCAGAGCCATGGGCTCCCCGAGGCTGCATCGTAGCTGTCTTTGCCATT  
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCCATGACTCCTTACCT  
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCTGCAGCACTGTT  
GCTATGATGATGCCGTCGTGCCCTTGGCCAGGACCCAGACGTGTGGAACTGCACCTTCAGA  
GTCTGCTTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACCAGAACTGCGA  
CTCAGCCCGGACCTCGGATGACAGGCTTTGTGCGAGTGTGAGCTTAATGGAACATCAGGGGAA  
CGATGACTCCTGGATTCTCCTTCCTGGGTGGGCTGGAGAAAGAGGCTGGTGTACCTGAGA  
TCTGGGATGCTGAGTGGCTGTTTGGGGGCCAGAGAAACACACTCAACTGCCCACTTCATT  
CTGTGACCTGTCTGAGGCCACCCCTGCAGCTGCCCTGAGGAGGCCACAGGTCCCCTTCTAG  
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCTCCTGAT  
GACCCCTATGGCCAACATCAACCCGGCACCACCCCAAGGCTGGCTGGGGAACCTTCACCCCT  
TCTGTGAGATTTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA  
TAAATTTATGTACTTTATAAATGAAAA

**FIGURE 82**

MAPRGCI VAVFAIFCISRL L CSHGAPVAPMTPYLMLCQPHKRCGDKFYDPLQHCCYDDAVVP  
LARTQTCGNCTFRVCFEQCCPWTFMVKLINQNCD SARTSDDR LCRSVS

**Signal peptide:**

amino acids 1-24

12345678910111213141516171819202122232425262728293031323334353637383940414243444546474849505152535455565758596061626364656667686970717273747576777879808182838485868788899091929394959697989910010110210310410510610710810911011111211311411511611711811912012112212312412512612712812913013113213313413513613713813914014114214314414514614714814915015115215315415515615715815916016116216316416516616716816917017117217317417517617717817918018118218318418518618718818919019119219319419519619719819920020120220320420520620720820921021121221321421521621721821922022122222322422522622722822923023123223323423523623723823924024124224324424524624724824925025125225325425525625725825926026126226326426526626726826927027127227327427527627727827928028128228328428528628728828929029129229329429529629729829930030130230330430530630730830931031131231331431531631731831932032132232332432532632732832933033133233333433533633733833934034134234334434534634734834935035135235335435535635735835936036136236336436536636736836937037137237337437537637737837938038138238338438538638738838939039139239339439539639739839940040140240340440540640740840941041141241341441541641741841942042142242342442542642742842943043143243343443543643743843944044144244344444544644744844945045145245345445545645745845946046146246346446546646746846947047147247347447547647747847948048148248348448548648748848949049149249349449549649749849950050150250350450550650750850951051151251351451551651751851952052152252352452552652752852953053153253353453553653753853954054154254354454554654754854955055155255355455555655755855956056156256356456556656756856957057157257357457557657757857958058158258358458558658758858959059159259359459559659759859960060160260360460560660760860961061161261361461561661761861962062162262362462562662762862963063163263363463563663763863964064164264364464564664764864965065165265365465565665765865966066166266366466566666766866967067167267367467567667767867968068168268368468568668768868969069169269369469569669769869970070170270370470570670770870971071171271371471571671771871972072172272372472572672772872973073173273373473573673773873974074174274374474574674774874975075175275375475575675775875976076176276376476576676776876977077177277377477577677777877978078178278378478578678778878979079179279379479579679779879980080180280380480580680780880981081181281381481581681781881982082182282382482582682782882983083183283383483583683783883984084184284384484584684784884985085185285385485585685785885986086186286386486586686786886987087187287387487587687787887988088188288388488588688788888989089189289389489589689789889990090190290390490590690790890991091191291391491591691791891992092192292392492592692792892993093193293393493593693793893994094194294394494594694794894995095195295395495595695795895996096196296396496596696796896997097197297397497597697797897998098198298398498598698798898999099199299399499599699799899910001001100210031004100510061007100810091010101110121013101410151016101710181019102010211022102310241025102610271028102910301031103210331034103510361037103810391040104110421043104410451046104710481049105010511052105310541055105610571058105910601061106210631064106510661067106810691070107110721073107410751076107710781079108010811082108310841085108610871088108910901091109210931094109510961097109810991100110111021103110411051106110711081109111011111112111311141115111611171118111911201121112211231124112511261127112811291130113111321133113411351136113711381139114011411142114311441145114611471148114911501151115211531154115511561157115811591160116111621163116411651166116711681169117011711172117311741175117611771178117911801181118211831184118511861187118811891190119111921193119411951196119711981199120012011202120312041205120612071208120912101211121212131214121512161217121812191220122112221223122412251226122712281229123012311232123312341235123612371238123912401241124212431244124512461247124812491250125112521253125412551256125712581259126012611262126312641265126612671268126912701271127212731274127512761277127812791280128112821283128412851286128712881289129012911292129312941295129612971298129913001301130213031304130513061307130813091310131113121313131413151316131713181319132013211322132313241325132613271328132913301331133213331334133513361337133813391340134113421343134413451346134713481349135013511352135313541355135613571358135913601361136213631364136513661367136813691370137113721373137413751376137713781379138013811382138313841385138613871388138913901391139213931394139513961397139813991400140114021403140414051406140714081409141014111412141314141415141614171418141914201421142214231424142514261427142814291430143114321433143414351436143714381439144014411442144314441445144614471448144914501451145214531454145514561457145814591460146114621463146414651466146714681469147014711472147314741475147614771478147914801481148214831484148514861487148814891490149114921493149414951496149714981499150015011502150315041505150615071508150915101511151215131514151515161517151815191520152115221523152415251526152715281529153015311532153315341535153615371538153915401541154215431544154515461547154815491550155115521553155415551556155715581559156015611562156315641565156615671568156915701571157215731574157515761577157815791580158115821583158415851586158715881589159015911592159315941595159615971598159916001601160216031604160516061607160816091610161116121613161416151616161716181619162016211622162316241625162616271628162916301631163216331634163516361637163816391640164116421643164416451646164716481649165016511652165316541655165616571658165916601661166216631664166516661667166816691670167116721673167416751676167716781679168016811682168316841685168616871688168916901691169216931694169516961697169816991700170117021703170417051706170717081709171017111712171317141715171617171718171917201721172217231724172517261727172817291730173117321733173417351736173717381739174017411742174317441745174617471748174917501751175217531754175517561757175817591760176117621763176417651766176717681769177017711772177317741775177617771778177917801781178217831784178517861787178817891790179117921793179417951796179717981799180018011802180318041805180618071808180918101811181218131814181518161817181818191820182118221823182418251826182718281829183018311832183318341835183618371838183918401841184218431844184518461847184818491850185118521853185418551856185718581859186018611862186318641865186618671868186918701871187218731874187518761877187818791880188118821883188418851886188718881889189018911892189318941895189618971898189919001901190219031904190519061907190819091910191119121913191419151916191719181919192019211922192319241925192619271928192919301931193219331934193519361937193819391940194119421943194419451946194719481949195019511952195319541955195619571958195919601961196219631964196519661967196819691970197119721973197419751976197719781979198019811982198319841985198619871988198919901991199219931994199519961997199819992000200120022003200420052006200720082009201020112012201320142015201620172018201920202021202220232024202520262027202820292030203120322033203420352036203720382039204020412042204320442045204620472048204920502051205220532054205520562057205820592060206120622063206420652066206720682069207020712072207320742075207620772078207920802081208220832084208520862087208820892090209120922093209420952096209720982099210021012102210321042105210621072108210921102111211221132114211521162117211821192120212121222123212421252126212721282129213021312132213321342135213621372138213921402141214221432144214521462147214821492150215121522153215421552156215721582159216021612162216321642165216621672168216921702171217221732174217521762177217821792180218121822183218421852186218721882189219021912192219321942195219621972198219922002201220222032204220522062207220822092210221122122213221422152216221722182219222022212222222322242225222622272228222922302231223222332234223522362237223822392240224122422243224422452246224722482249225022512252225322542255225622572258225922602261226222632264226522662267226822692270227122722273227422752276227722782279228022812282228322842285228622872288228922902291229222932294229522962297229822992300230123022303230423052306230723082309231023112312231323142315231623172318231923202321232223232324232523262327232823292330233123322333233423352336233723382339234023412342234323442345234623472348234923502351235223532354235523562357235823592360236123622363236423652366236723682369237023712372237323742375237623772378237923802381238223832384238523862387238823892390239123922393239423952396239723982399240024012402240324042405240624072408240924102411241224132414241524162417241824192420242124222423242424252426242724282429243024312432243324342435243624372438243924402441244224432444244524462447244824492450245124522453245424552456245724582459246024612462246324642465246624672468246924702471247224732474247524762477247824792480248124822483248424852486248724882489249024912492249324942495249624972498249925002501250225032504250525062507250825092510251125122513251425152516251725182519252025212522252325242525252625272528252925302531253225332534253525362537253825392540254125422543254425452546254725482549255025512552255325542555255625572558255925602561256225632564256525662567256825692570257125722573257425752576257725782579258025812582258325842585258625872588258925902591259225932594259525962597259825992600260126022603260426052606260726082609261026112612261326142615261626172618261926202621262226232624262526262627262826292630263126322633263426352636263726382639264026412642264326442645264626472648264926502651265226532654265526562657265826592660266126622663266426652666266726682669267026712672267326742675267626772678267926802681268226832684268526862687268826892690269126922693269426952696269726982699270027012702270327042705270627072708270927102711271227132714271527162717271827192720272127222723272427252726272727282729273027312732273327342735273627372738273927402741274227432744274527462747274827492750275127522753275427552756275727582759276027612762276327642765276627672768276927702771277227732774277527762777277827792780278127822783278427852786278727882789279027912792279327942795279627972798279928002801280228032804280528062807280828092810281128122813281428152816281728182819282028212822282328242825282628272828282928302831283228332834283528362837283828392840284128422843284428452846284728482849285028512852285328542855285628572858285928602861286228632864286528662867286828692870287128722873287428752876287728782879288028812882288328842885288628872888288928902891289228932894289528962897289828992900290129022903290429052906290729082909291029112912291329142915291629172918291929202921292229232924292529262927292829292930293129322933293429352936293729382939294029412942294329442945294629472948294929502951295229532954295529562957295829592960296129622963296429652966296729682969297029712972297329742975297629772978297929802981298229832984298529862987298829892990299129922993299429952996299729982999300030013002300330043005300630073008300930103011301230133014301530163017301830193020302130223023302430253026302730283029303030313032303330343035303630373038303930403041304230433044304530463047304830493050305130523053305430553056305730583059306030613062306330643065306630673068306930703071307230733074307530763077307830793080308130823083308430853086308730883089309030913092309330943095309630973098309931003101310231033104310531063107310831093110311131123113311431153116311731183119312031213122312331243125312631273128312931303131313231333134313531363137313831393140314131423143314431453146314731483149315031513152315331543155315631573158315931603161316231633164316531663167316831693170317131723173317431753176317731783179318031813182318331843185318631873188318931903191319231933194319531963197319831993200320132023203320432053206320732083209321032113212321332143215321632173218321932203221322232233223432253226322732283229323032313232323332343235323632373238323932403241324232433244324532463247324832493250325132523253325432553256325732583259326032613262326332643265326632673268326932703271327232733274327532763277327832793280328132823283328432853286328732883289329032913292329332943295329632973298329933003301330233033

**FIGURE 83**

GGGGGCGGGTGCCTGGAGCACGGCGCTGGGGCCGCCGACGCTCACTCGCTCGCACTCAG  
 TCGCGGGAGGCTTCCCCGCGCCGGCCGCTCCCGCCGCTCCCGGCACACAGAAGTTCCTCT  
 GCGCGTCCGACGGCGACATGGGCGTCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGGA  
 TCCCTGCTCTTCGCTCTCTTCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTTCAAGTTCG  
 CACGCCGATATTCCTGTATGTCTGTCCCAGGGGCAGAACGTACCCCTCACCTGCAGGCTCT  
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTTCTACAAGACGTGGTACCGCAGCTCGAGG  
 GCGAGGTGCAGACCTGCTCAGAGCGCCGGCCCATCCGCAACCTCACGTTCCAGGACCTTCA  
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTCAGCGCCACGGGC  
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCCCTGCTG  
 GATAGCGGCCTCTACTGCTGCCTGGTGGTGGAGATCAGGCACCACCACTCGGAGCACAGGGT  
 CCATGGTGCCATGGAGCTGCAGGTGCAGACAGGCAAAGATGCACCATCCAACCTGTGTGGTGT  
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC  
 ATCGTAGGAATCCTCTGCCTCCCCCTCATCTGCTCCTGGTCTACAAGCAAAGGCAGGCAGC  
 CTCGAACCGCCGTGCCAGGAGCTGGTGGGATGGACAGCAACATTCAAGGGATTGAAAACC  
 CCGGCTTTGAAGCCTCACCACTGCCAGGGGATACCGAGGCCAAAGTCAGGCACCCCTG  
 TCCTATGTGGCCAGCGGCAGCCTTCTGAGTCTGGCGGCATCTGCTTTGAGAGCCAGCAC  
 CCCCCGTCTCCTCCAGGCCCGGAGACGTCTTCTTCCCATCCCTGGACCTGTCCCTGACT  
 CTCAAAACCTTGAAGTCACTCTAGCCCAGCTGGGGGACAGTGGGCTGTTGTGGCTGGGTCTGG  
 GGCAGGTGCATTTGAGCCAGGGCTGGCTCTGTGAGTGGCCTCCTTGGCCTCGGCCCTGGTTC  
 CCTCCTCCTGCTCTGGGCTCAGATACTGTGACATCCAGAAGCCAGCCCTCAACCCCTC  
 TGGATGCTACATGGGGATGCTGGACGGCTCAGCCCTGTTCCAAGGATTTTGGGTGCTGAG  
 ATTCTCCCCTAGAGACCTGAAATTCACAGCTACAGATGCCAAATGACTTACATCTTAAGAA  
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTCGTTCTGAGACATGAGCCTTGGGATGTGGCA  
 GCATCAGTGGGACAAGATGGACACTGGGGCCACCTCCAGGCACCAGACACAGGGCACGGTG  
 GAGAGACTTCTCCCCGTGGCCGCCCTGGCTCCCCCGTTTGGCCGAGGTGCTTCTCTGTC  
 AGACTTCCTCTTTGTACCACAGTGGCTCTGGGGCCAGGCCTGCCTGCCCACTGGCCATCGCC  
 ACCTTCCCAGCTGCCTCCTACCAGCAGTTTCTCTGAAGATCTGTCAACAGGTTAAGTCAAT  
 CTGGGGCTTCCACTGCCTGCATTCCAGTCCCAGAGCTTGGTGGTCCCGAAACGGGAAGTAC  
 ATATTGGGGCATGGTGGCCTCCGTGAGCAAAATGGTGTCTTGGGCAATCTGAGGCCAGGACAG  
 ATGTTGCCCAACCACTGGAGATGGTGTCTGAGGAGGTGGGTGGGGCCCTTCTGGGAAGGTGA  
 GTGGAGAGGGGCACCTGCCCCCGCCCTCCCATCCCTACTCCCACTGCTCAGCGCGGGCC  
 ATTGCAAGGGTGCCACACAATGTCTTGTCCACCTGGGACACTTCTGAGTATGAAGCGGGAT  
 GCTATTAAAACTACATGGGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAGA

**FIGURE 84**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897  
><subunit 1 of 1, 311 aa, 1 stop  
><MW: 33908, pI: 6.87, NX(S/T): 6  
MGVPTALEAGSWRWGSLFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVVK  
GHDVTFYKTWYRSSRGEVQTCSERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLASD  
HHGNFSITMRNLTLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNVCVYPSSSQ  
DSENITAAALATGACIVGILCLPLILLLVYKQRQAASNRRQAQLVRMDSNIQGIENPGFEAS  
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPGPGDVFFPSLDPVPDSPNFEVI

**Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 190-216

**FIGURE 85**

CCCACGCGTCCGCGCCTCTCCCTTCTGCTGGACCTTCCTTCGTCTCTCCATCTCTCCCTCCT  
 TTCCCGCGTTCTCTTTCCACCTTTCTCTTCTTCCACCTTAGACCTCCCTTCTCGCCCTCC  
 TTTCTGCCCACCGTGCTTCTTGGCCCTTCTCCGACCCCGCTCTAGCAGCAGACCTCCTGG  
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTTTCGTCTCCCTTCTCCCGA  
 CTCGCTCCCGGACCAGCGGCTGACCCTGGGGAAGGATGGTTCCTCCGAGGTGAGGGTCTCT  
 TCCTCCTTGTGCGGACTCGCGCTGTCTGTGTTCCCTTGGACTCCACGCTCGAGCCGCGCC  
 AGACATGTTCTGCCTTTTCCATGGGAAGAGATACTCCCCGCGCAGAGCTGGCACCCCTACT  
 TGGAGCCACAAGGCCTGATGTACTGCCTGCCTGTACCTGCTCAGAGGGCGCCCATGTGAGT  
 TGTTACCGCTCCACTGTCCGCTGTCCACTGCCCCAGCCTGTGACGGAGCCACAGCAATG  
 CTGTCCCAAGTGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAGTCTGCC  
 AGCACAACGGGACCATGTACCAACACGGAGAGATCTTCAGTGCCCATGAGCTGTTCCCTCC  
 CGCTGCCCAACCAAGTGTGTCTCTGCAGCTGCACAGAGGGCCAGATCTACTGCGGCTCAC  
 AACCTGCCCCGAACCAAGGTGCCAGCACCCCTCCCACTGCCAGACTCCTGCTGCCAAGCCT  
 GCAAAGATGAGGCAAGTGAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGGTG  
 AGACATCCTCAGGATCCATGTTCCAGTGATGCTGGGAGAAAAGAGAGGGCCGGGCACCCAGC  
 CCCCCTGGCCTCAGCGCCCTCTGAGCTTCATCCCTCGCCACTTCAGACCCAAGGGAGCAG  
 GCAGCACAACGTCAAGATCGTCCTGAAGGAGAAAACATAAGAAAGCCTGTGTGCATGGCGG  
 AAGACGTACTCCACGGGGAGGTGTGGCACCCGGCTTCCGTGCCTTCGGCCCTTGCCCTG  
 CATCCTATGCACCTGTGAGGATGGCCGCCAGGACTGCCAGCGTGTGACCTGTCCACCGAGT  
 ACCCTGCCGTACCCCCGAGAAAGTGGCTGGGAAGTGTGCAAGATTTGCCAGAGGACAAA  
 GCAGACCTTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCCAAGGCACCGGGCCGGTCTT  
 CGTCCACACATCGGTATCCCCAAGCCAGACAACCTGCGCTCGCTTTGCCCTGGAACACGAGG  
 CCTCGGACTTGGTGGAGATCTACCTCTGGAAGCTGGTAAAAGATGAGGAACTGAGGCTCAG  
 AGAGGTGAAGTACCTGGCCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCAAGA  
 AAGTCAGGAAGCAAGACTTCAGAAAGAGGCACAGCACTTCCGACTGCTCGCTGGCCCCAC  
 GAAGGTCACTGGAACGTCTTCTAGCCCAGACCCTGGAGCTGAAGGTACAGGCCAGTCCAGA  
 CAAAGTGACCAAGACATAACAAAGACCTAACAGTTGCAGATATGAGCTGTATAATTGTTGTT  
 ATTATATATTAATAAATAAGAAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 86**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSLLGLALLWFPLDSHARAPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFP SRLPNQCVLCSCTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVVRHPQDPCSSDAGRKRGGT PAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPK VAGKC
CKICPEDKADPGHSEISSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKL V
KDEETEAQRGEVPGPRPHSQNLPLDSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

**Signal peptide:**

amino acids 1-25







**FIGURE 89**

**FIGURE 90**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905  
<subunit 1 of 1, 406 aa, 1 stop  
<MW: 46038, pI: 6.50, NX(S/T): 2  
MGPSTPLILFLLSWSGFLQGGHHLVEYMERRLAALAEERLAQCQDQSSRHAAELRDFKNKM  
LPILLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR  
RNEKYDMVTDGTYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPRL  
RDFTLAMAARKASRVRFPPWVGTLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN  
RTVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCIAKLDPQTLDTAQ  
QWDTPCPRENAEAAFCVTLYVVYNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH  
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEV

**Important features:****Signal peptide:**

amino acids 1-21

**N-glycosylation sites.**

amino acids 177-180, 248-251

**FIGURE 91**

GACAGCTGTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTTGCCCTCCGCTCACGCAG  
 AGCCTCTCCGTGGCTTCCGCACCTTGAGCATTAGGCCAGTTCTCCTCTCTCTAATCCAT  
 CCGTCACCTCTCCTGTCATCCGTTTCCATGCCGTGAGGTCCATTACAGAACACATCC**ATGG**  
 CTCTCATGCTCAGTTTGGTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTTT  
 GGGCCAGACAAGCCTGTCCAGGCCTTGGTGGGGAGGACGCAGCATTCTCCTGTTTCTCTGTC  
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCGGTTCTTCAGGGGCCAGTTCTCTAGCGTGG  
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTTATGCAGATGCCACAGTATCAAGGCAGG  
 ACAAACCTGGTGAAGGATTCTATTGCGGAGGGGCGCATCTCTCTGAGGCTGAAAAACATTAC  
 TGTGTTGGATGCTGGCCTCTATGGGTGCAGGATTAGTTCCCAGTCTTACTACCAGAAGGCCA  
 TCTGGGAGCTACAGGTGTGAGCACTGGGCTCAGTTCCTCTCATTTCCATCACGGGATATGTT  
 GATAGAGACATCCAGCTACTCTGTCTAGTCCCTCGGGCTGGTTCCCCGGGCCACAGCGAAGTG  
 GAAAGGTCACAAGGACAGGATTGTCCACAGACTCCAGGACAACAGAGACATGCATGGCC  
 TGTGTTGATGTGGAGATCTCTGTACCGTCCAAGAGAACGCCGGGAGCATATCCTGTTCCATG  
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACCTTTTTCGA  
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGGAATACTCTGCTGTGGCCTATTTTTTG  
 GCATTGTTGGACTGAAGATTTTCTCTCCAAATTCAGTGGAATAATCCAGGCGGAAGTGGAC  
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGAAACACGCAGTGGAGGTGAC  
 TCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTCTGATCTGAAAAGTGAACCCATA  
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTTACAAGGAAGAGTGTGGTGGCT  
 TCTCAGAGTTTCCAAGCAGGGAACATTACTGGGAGGTGGACGGAGGACAAATAAAAGGTG  
 GCGCGTGGGAGTGTGCCGGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTTGTCTCCCG  
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTTGTATTTACATTAAATCCCCGT  
 TTTATCAGCGTCTTCCCCAGGACCCACCTACAAAAATAGGGGTCTTCTGGACTATGAGTG  
 TGGGACCATCTCCTTCTTCAACATAAATGACCAGTCCCTTATTTATACCTGACATGTCGGT  
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCTTATAATGAGCAAAATGGAAGTCCC  
 ATAGTCATCTGCCAGTCAACCAGGAATCAGAGAAAGAGGCCCTCTGGCAAAGGCCCTCTGC  
 AATCCAGAGACAAGCAACAGTGAGTCTCCTCACAGGCAACCCAGCCCTTCTCTCCAGGG  
 GTGAAATG**TAGG**ATGAATCAGATCCACATTTCTTTTAGGGATATTAAAGGTCTCTCTCCCA  
 GATCCAAAGTCCCGCAGCAGCCCGCAAGGTGGCTTCCAGATGAAGGGGACTGGCCTGTCC  
 ACATGGGAGTCAGGTGTCTGCTGCGCTGAGCTGGGAGGGAAGAGGCTGACATTACATTT  
 AGTTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG  
 TCAGGAATTTCCATCTCACAGGCTGTGGTGATTAAGTAGACAAGGAATGTGAATAATGC  
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTTGTTCATTATATTACACTTTCAGTA  
 AAAAAA

**FIGURE 92**

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAAFCFLSPKTNAEAMEVRRFFRGQFSS  
 VVHLYRDGKDQPFMQMPQYQGR TKLVKDSIAEGRISLRLENITVLDAGLYGCRIS SQSYQK  
 AIWELQVSALGSVPLISITGYVDRDIQLLCQSSGWFRPTAKWKGPQGDLSTDSRTNRDMH  
 GLFDVEISLTVQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF  
 FGIVGLKIFFSKFQWKIQAE LDWR RKHGQAE LRDARKH AVEVTLDPETAHPKLCVSDLKTVT  
 HRKAPQEVFHSKRFRTRKSVVASQS FQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTLS  
 PDHGYWVLR LINGEHL YFTLNPRFISVFPRT PPTKIGVFLDYECGTISFFNINDQSLIYTLTC  
 RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSSESSQATT PFLP  
 RGEN

**Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 239-255

**FIGURE 93**

GCGATGGTGC GCCCGGTGGCGGTGGCGGGCGCGGTTGCGGAGGCTTCCTTGGTCGGATTGCA  
 ACGAGGAGAGATGACTGACCAACCGACTGGCTGAATGAATGAATGGCGGAGCCGAGCGCGC  
**CATGAGGAGCCTGCCGAGCCTGGCGGCCCTCGCCCTGTGTGCTGCGCCGCCGCCGCCGCCG**  
 CCGTCGCCTCAGCCGCCCTCGGCGGGGAATGTCACCGTGGCGCGCGGGCCCGGGGGAGGTG  
 GACGCGTCGCCGGGCCCCGGGTTGCGGGGCGAGCCAGCCACCCCTTCCTTAGGGCGACGGC  
 TCCCACGGCCGAGGCCCGGAGACCGGGCCCCCGCGCGCCACCGTCCACCGACCCCTGGCTG  
 CGACTTCTCCAGCCAGTCTCCCGGAGACCACCCCTCTTTGGCGACTGCTGGACCCCTCTTC  
 ACCACCTTTCAGGCGCGCTCGGCCCTCGCCGACCACCCCTCCGCGCGCGGAACGCACCTC  
 GACCACCTCTCAGGCGCCGACCGAGACCCGCGCCGACCAACCCCTTCGACGACCACTGGCCCGG  
 CGCCGACCAACCCCTGTAGCGACCAACCGTACCGCGCGCCACGACTCCCGGAGCCCGACCCCTC  
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCTCTCCACCCCACTGCCACCGAGGCCCCCTC  
 TTCGCTCTCTCAGAGTATGTATGTAACCTGCTCTGTGGTTGGAAGCCTGAATGTGAATCGCT  
 GCAACCAGACCACAGGGCAGTGTGAGTGTGCGCCAGGTTATCAGGGGCTTCACCTGTGAAACC  
 TGCAAGAGGGCTTTTACCTAAATTACACTTCTGGGCTCTGTAGCCATGTGACTGTAGTCC  
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GCAACAGAGGGTGGAACCTGAAGTTTATT  
 TTATTTTAGCAAGGGAAGGCTGCTACTCTCAAGGACCATACTGGTTTAAACAAAG  
 GAGGATGAGGGTCATAGATTTACAAAATATTTATATACCTTTATTCTCTACTTTTATATGT  
 TATATTTAATGTCAAGGATTTAAACATCTAATTTACTGATTAGTCTCTCAAAGCAGTAG  
 AGTCGCAATTTTCTCTGGGATAATTTCTGTAATTTCAAGGAAATTTATGAAGAAT  
 AAATCTGCTTTTCTGGAAGGCTTTCAGGCATGAAACCTGCTAGGAGGTTTAGAAATGTTCTT  
 ATGTTTATTAATATACCATTTGGAGTTTGAGGAATTTGTTGTTGGTTTATTTTCTCTCTA  
 ATCAAAATTTCTACATTTGTTTCTTTGGACATCTAAAGCTTAACCTGGGGGTACCCATTTTA  
 TTTAAGTAGTGGAAGTAGACTGGTTTTACTCTATTTACCAGTACATTTTGGAGCAAAAAG  
 TAGATTAAGCAGGAATATCTTTAACTATTATGTTATTTGGAGGTAATTTAATCTAGTGA  
 ATAATGTACTGTTATCTAAGCATTTGCCTTGACTGCACGTAAAGTAATTTATCTTTGACCT  
 TATGTGAGGCACTTTGGCTTTTGTGGACCCCAAGTCAAAAACCTGAAGAGACAGTATTAAT  
 AATGAAAAAATAATGACAGGTTATACTAGTGAACCTGGGTATAACCAAGATCTGCTGC  
 CACTTACGAGCTGTGTTCTTTGGGCAAGTAATTTCTTTCACTGAGCTTGTCTTCTCAAG  
 GTTGTGTGAAGATTAAATGAGTGTATATATATAAATGCCTAGCACATGTCACTCAATAAA  
 TTCTGTTTTGTTTTAATTTCAAAGGAATATTATGGACTGAAATGAGAGAACATGTTTTAAGA  
 ACTTTTAGCTCCTTGACAAAGAAGTGCTTTATACTTTAGCACTAAATATTTAAATGCTTTA  
 TAAATGATATTATACCTGTTATGGAATATTGTATCATATTGTAGTTTATTAATAATGTAGAAG  
 AGGCTGGGCGCGGTGGCTCACGCCTGTAATCCTAGCACTTTGGGAGGCCAAGCGGGTGGAT  
 CACTTGAGGCCAGGAGTTCTAGATGAGCCTGGCCAGCACAGTGAACCCCGCTCTACTAAA  
 AATACAAACAAATTAGCTGGGCGTGGTGGCACACACCTGTAGTCCGAGTCTCGGGAGGCT  
 GAGGCAGGAGAATCGGTTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGCGCACCT  
 GCACTCCAGCCTGGTGAGAGAGGGAGACTCTGTCTTAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 94**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLSLGLGALLCCAAAAAASASAASAGNVTGGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPETTPWATAGPSSTTFQAPLGPSPPTPPAAERTS
TTSQAPTRPAPTTLSTTTGPAPTTVPATTVPAPTTPTPTPDLPSSSSSSVLPTPPATEAPS
SPPPEYVCNCSSVVGSLNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**N-glycosylation sites.**

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

**EGF-like domain cysteine pattern signature.**

amino acids 214-226.

**FIGURE 95**

TGCGGCGCAGTGTAGACCTGGGAGG**ATG**GGCGGCCTGCTGCTGGCTGCTTTTCTGGCTTTGG  
TCTCGGTGCCAGGGCCCAGGCCGTGTGGTTGGGAAGACTGGACCCTGAGCAGCTTCTTGGG  
CCCTGGTACGTGCTTGCGGTGGCCTCCCGGGAAAAGGGCTTTGCCATGGAGAAGGACATGAA  
GAACGTCGTGGGGGTGGTGGTGACCCCTCACTCCAGAAAAACAACCTGCGGACGCTGTCCTCTC  
AGCACGGGCTGGGAGGGTGTGACCAGAGTGTGATGGACCTGATAAAGCGAAACTCCGGATGG  
GTGTTTGAGAATCCCTCAATAGCGGTGCTGGAGCTCTGGGTGCTGGCCACCAACTTCAGAGA  
CTATGCCATCATCTTCACTCAGCTGGAGTTCGGGGACGAGCCCTTCAACACCGTGGAGCTGT  
ACAGTCTGACGGAGACAGCCAGCCAGGAGGCCATGGGGCTCTTCACCAAGTGGAGCAGGAGC  
CTGGGCTTCCTGTACAG**TAG**CAGGCCCAGCTGCAGAAGGACCTCACCTGTGCTCACAAAGAT  
CCTTCTGTGAGTGTGCGTCCCCAGTAGGGATGGCGCCACAGGGTCCTGTGACCTCGGCCA  
GTGTCCACCCACCTCGCTCAGCGGCTCCCGGGGCCAGCACCAGCTCAGAATAAAGCGATT  
CACAGCA

**FIGURE 96**

MGGLLLAAFLALVSVPRQAQAVLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT  
LTPENNLRTLSSQHGLGGCDQSVMDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL  
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20



**FIGURE 97**

AACAGACGTTCCCTCGCGCCCTGGCACCTCTAACCCAGAC**ATG**CTGCTGCTGCTGCTGCC  
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAACTGCTGACGATGCAGAGTT  
 CCGTGACGGTGCAGGAAGGCCTGTGTGCCATGTGCCCTGCTCCTTCTCCTACCCCTCGCAT  
 GGCTGGATTTACCCTGGCCAGTAGTTTCATGGCTACTGGTTCCGGGAAGGGCCAATACAGA  
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTCGGGCAGTGTGGGAGGAGACTCGGGACC  
 GATTCACCTCTCTGGGGACCCACATACCAAGAATTGCACCTGAGCATCAGAGATGCCAGA  
 AGAAGTGATGCGGGGAGATACTTCTTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA  
 ACATCACCGGCTCTCTGTGAATGTGACAGCCTTGACCCACAGGCCAACATCCTCATCCCAG  
 GCACCCTGGAGTCCGGCTGCCCCAGAATCTGACCTGCTCTGTGCCCTGGGCCCTGTGAGCAG  
 GGGACACCCCTATGATCTCTGGATAGGGACCTCCGTGTCCCCCTGGAGCCCTCCACCAC  
 CCGCTCCTCGGTGCTCACCTCATCCACAGCCCCAGGACCATGGCACCAGCCTCACCTGTC  
 AGGTGACCTTCCCTGGGGCCAGCGTGACCACGAACAAGACCGTCCATCTCAACGTGTCCTAC  
 CCGCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTTGGG  
 AAATGGCTCATCTGTGTCACCTCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGCAGTTGATG  
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCTGTGCCCC  
 TCACAGCCCTCAAACCGGGGGTGTGGAGCTGCCTTGGGTGCACCTGAGGGATGCAGCTGA  
 ATTACCTGCAGAGCTCAGAACCCTCTCGGCTCTCAGCAGGTCTACCTGAACGTCTCCCTGC  
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTGGGGGAGCTGGAGCCACAGCCCTG  
 GTCTTCTGTCTTCTGCGTCATCTTCTGTGTAGTGAGGTCTGCAGGAAGAAATCGGCAAG  
 GCCAGCAGCGGGCGTGGGAGATACGGGCATAGAGGATGCAAACGTGTGAGGGGTTACGCT  
 CTCAGGGGCCCCTGACTGAACCTTGGGCAGAAGACAGTCCCCAGACCAGCCTCCCCAGCT  
 TCTGCCCCGTCTCTCAGTGGGGGAAGGAGAGCTCCAGTATGCATCCCTCAGCTTCCAGATGGT  
 GAAGCCTTGGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC  
 ACAGAT**TGA**GAAATGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGCAAGGGA  
 GAAGTCAGAGGCTGATTCTTGTAGAATTAACAGCCCTCAACGTGATGAGCTATGATAACACT  
 ATGAATTATGTGCAGAGTGAAAGCACACAGGCTTTAGAGTCAAAGTATCTCAAACCTGAAT  
 CCACACTGTGCCCTCCCTTTTATTTTTTAACTAAAAGACAGACAAATTCCTA

**FIGURE 98**

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPCSFSPSHGWIYPGPVVHGYWF  
 REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTLSIRDARRSDAGRYFFRMEKG  
 SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCVWPWACEQGTPPMISWIGTSVS  
 PLDPSTTRSSVLTLPQPQDHGTS LTCQVTFPGASVTNKTVHLNVSYPPQNLTMTVFQGDG  
 TVSTVLGNGSSLSLPEGQSLRLVCAVDAVDSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV  
 HLRDAAEFTCRAQNPLGSQQVYLVNLSLQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVRS  
 CRKKSARPAAGVGDGTGIEDANAVRGSSASQGPLETPWAEDSPPDQPPPPASARSSVGEGLQYA  
 SLSFQMKPWDSRGQEATDTEYSEIKIHR

**Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 351-370

**FIGURE 99**

GACGCCCAGTGACCTGCCGAGGTCGGCAGCACAGAGCTCTGGAG**ATG**AAGACCCTGTTCTCTG  
GGTGTACGCTCGGCCTGGCCGCTGCCCTGTCTTCACCCTGGAGGAGGAGGATATCACAGG  
GACCTGGTACGTGAAGGCCATGGTGGTCGATAAGGACTTTCGGGAGGACAGGAGGCCAGGA  
AGGTGTCCCAGTGAAGGTGACAGCCCTGGGCGGTGGGAAGTTGGAAGCCACGTTACCTTC  
ATGAGGGAGGATCGGTGCATCCAGAAGAAAATCCTGATGCGGAAGACGGAGGAGCCTGGCAA  
ATACAGCGCCTATGGGGGCAGGAAGCTCATGTACCTGCAGGAGCTGCCCAGGAGGGACCACT  
ACATCTTTTACTGCAAAGACCAGCACCATGGGGGCCCTGCTCCACATGGGAAAGCTTGTGGGT  
AGGAATTCTGATACCAACCGGAGGCCCTGGAAGAATTTAAGAAATTGGTGCAGCGCAAGGG  
ACTCTCGGAGGAGGACATTTTCAGCCCCCTGCAGACGGGAAGCTGCGTTCCCGAACAC**TAGG**  
CAGCCCCCGGCTGTGCACCTCCAGAGCCCACCCTACCACCAGACACAGAGCCCGGACCACCT  
GGACCTACCCTCCAGCCATGACCCCTCCCTGCTCCCACCCACCTGACTCCAAATAAAGTCCT  
TTTCCCCCAA

**FIGURE 100**

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTFLGLGVTGLAAALSFTLEEDITGTWYVKAMVVDKDFPEDRRPRKVS PVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSA YGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREAL EEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

**Important features:****Signal peptide:**

amino acids 1-17

**FIGURE 101**

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC  
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC**ATG**AGGATTCGCAGTTAA  
 TCCTGCTTGCTCTGGCAACAGGGCTTGTAGGGGAGAGACCAGGATCATCAAGGGGTTGAG  
 TGCAAGCCTCACTCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG  
 GCGGACGCTCATCGCCCCAGATGGCTCCTGACAGCAGCCCACTGCCTCAAGCCCCGTACA  
 TAGTTCACCTGGGGCAGCACAACTCCAGAAGGAGGAGGCTGTGAGCAGACCCGGACAGCC  
 ACTGAGTCCTTCCCCACCCCGGCTTCAACAACAGCCTCCCCAACAAGACCACCGCAATGA  
 CATCATGCTGGTGAAGATGGCATCGCCAGTCTCCATCACCTGGGCTGTGCGACCCCTCACCC  
 TCTCCTCACGCTGTGTCACTGCTGGCACCAGCTGCCTCATTTCCGGCTGGGGCAGCACGTCC  
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCGATGCGCCAACATCACCATCATTGAGCACCA  
 GAAGTGTGAGAACGCCTACCCCGCAACATCACAGACACCATGGTGTGTGCCAGCGTGCAGG  
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGGCCCTCTGGTCTGTAACCACTCTCTT  
 CAAGGCATTATCTCCTGGGGCCAGGATCCGTGTGCGATCACCCGAAAGCCTGGTGTCTACAC  
 GAAAGTCTGCAAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAT**TAG**ACTGGACCCA  
 CCCACCACAGCCCATCACCTCCATTCCACTTGGTGTGGTTCCTGTTCACTCTGTAAAT  
 AAGAAACCTTAAGCCAAGACCTCTACGAACATTCTTTGGGCCTCCTGGACTACAGGAGATG  
 CTGTCACTTAATAATCAACCTGGGGTTGAAATCAGTGAGACCTGGATTCAAATTTCTGCCTT  
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTTGTCTCTGTTATCCCCAGCCCCA  
 AAGACAGCTCCTGGCCATATATCAAGGTTTCAATAAATATTGCTAAATGAAAAAAAAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 102**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQPWQAALFEKTRLLCGATLIAPRWLLTAAH
CLKPRYIVHLGQHNLQKEEGCEQTRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVITAGTSCGISGWGSTSSPQLRLPHTLRCANITIIIEHQKCNAYPGNITDTM
VCASVQEGGKDCSCQDSSGGPLVCNQLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN

```

**Important features:****Signal peptide:**

amino acids 1-18

**Serine proteases, trypsin family, histidine active site.**

amino acids 58-63

**N-glycosylation sites.**

amino acids 99-102, 165-168, 181-184, 210-213

**Glycosaminoglycan attachment site.**

amino acids 145-148

**Kringle domain proteins.**

amino acids 197-209, 47-64

**Serine proteases, trypsin family, histidine protein**

amino acids 199-209, 47-63, 220-243

**Apple domain proteins**

amino acids 222-249, 189-222

**FIGURE 103**

GAGCAGTGTTCGTCTGGAGCCGATGCCAAAAACCATGCATTTCTTATTAGATTTCATTGTTT  
TCTTTTATCTGTGGGGCCTTTTACTGCTCAGAGACAAAAGAGAGGAGAGCACCGAAGAA  
GTGAAATAGAAAGTTTTCATCGTCCAGAAAAGTCTCTAAGACAAGCAAGAAGGGAGACCT  
ACTAAATGCCCATTATGACGGCTACCTGGCTAAAGACGGCTCGAAATTCCTACTGCAGCCGGA  
CACAAAATGAAGGCCACCCCAAATGGTTTGTTCTTGGTGTTGGGCAAGTCATAAAAGGCCTA  
GACATTGCTATGACAGATATGTGCCCTGGAGAAAAGCGAAAAGTAGTTATACCCCCCTTCATT  
TGCATACGAAAGGAAGGCTATGCAGAAGGCAAGATTCCACCGGATGCTACATTGATTTTTG  
AGATTGAACTTTATGCTGTGACCAAAGGACCACGGAGCATTGAGACATTTAAACAAATAGAC  
ATGGACAATGACAGGCAGCTCTCTAAAGCCGAGATAAACCTCTACTTGCAAAGGGAATTTGA  
AAAAGATGAGAAGCCACGTGACAAGTCATATCAGGATGCAGTTTTAGAAGATATTTTAAGA  
AGAATGACCATGATGGTGATGGCTTCATTTCTCCCAAGGAATACAATGTATACCAACACGAT  
GAACTATAGCATATTTGTATTTCTACTTTTTTTTTTTAGCTATTTACTGTACTTTATGTATA  
AAACAAAGTCATTTTCTCCAAGTTGTATTTGCTATTTTCCCCATGAGAAGATATTTTGA  
TCTCCCCAATACATTGATTTTGGTATAATAATGTGAGGCTGTTTGGCAAACCTTAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 104**

```

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSTSKKGDLLNAHYDG
YLAkdGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGKRRVVIPPSFAYGKEGY
AEGKIPDPATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDGFISPKYENVYQHDEL

```

**Important features:****Endoplasmic reticulum targeting sequence.**

amino acids 219-222

**N-glycosylation site.**

amino acids 45-48

**FKBP-type peptidyl-prolyl cis-trans isomerase**

amino acids 87-223, 129-142

**EF-hand calcium-binding domain proteins**

amino acids 202-214, 195-214



**FIGURE 105**

CAGAAATGCAGGGACCATTGCTTCTTCCAGGCCTCTGCTTTCTGCTGAGCCTCTTTGGAGCT  
 GTGACTCAGAAAACCAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA  
 CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGGCAGAACTATTCACATTCC  
 CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTGTAATCCCAGTTCTTTGGGAAG  
 CCAAGGCAGGTGGATCACCTGAGGTGAGGAGTTTGAGACCAGCCTGGCCAACATAGTGAAAC  
 CCCGTGTCTACTAAAAATACAAAATCAGCCGGGCGTGGTGGTGCATGCCTGCAATCCCAGT  
 TACTCGGAGGCTGAGGCAGGAGAATCGCTTGAACCTCAGGAGGCAGAAGTTGCAGTGAACCC  
 AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA  
 TAGTTTCTTGTTTCATTTCGCGACTGCCCTCTCAGTGTTCCTGGGATCCCCTCCCAAATAA  
 AGTACTTATATTCTC

**FIGURE 106**

MQGPILLPLGLCFLLSLFGAVTQKTKTSCAKCPPNASCVNNTHCTCNHGYTSGSGQKLFTFEL  
ETCNARHGG SRL

**Signal peptide:**

amino acids 1-18

106/249

**FIGURE 107**

CAAGCAGGTCATCCCCTTGGTGACCTTCAAAGAGAAGCAGAGAGGGGCAGAGGTGGGGGGGCAC  
 AGGGAAAGGGTGACCTCTGAGATTCCCCTTTTCCCCCAGACTTTGGAAGTGACCCACC**ATGG**  
 GGCTCAGCATCTTTTTGCTCCTGTGTGTTCTTGGGCTCAGCCAGGCAGCCACCCGAAGATT  
 TTCAATGGCACTGAGTGTGGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTTGAGGGCAC  
 CAGCCTGCGCTGCGGGGGTGTCTTATTGACCACAGGTGGGTCTCACAGCGGCTCACTGCA  
 GCGGCAGCAGGTACTGGGTGCGCCTGGGGGAACACAGCCTCAGCCAGCTCGACTGGACCCGAG  
 CAGATCCGGCACAGCGGCTTCTCTGTGACCCATCCCGGCTACCTGGGAGCCTCGACGAGCCA  
 CGAGCAGACCTCCGGCTGCTGCGGCTGCGCCTGCCCGTCCGCGTAACCAGCAGCGTTCAAC  
 CCCTGCCCTGCCCAATGACTGTGCAACCGCTGGCACCAGTGCACGTCTCAGGCTGGGGC  
 ATCACCACCCACCCACGGAACCCATTCCCGGATCTGCTCCAGTGCCCTCAACCTCTCCATCGT  
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG  
 GCGGCGTCCCGGGGCAGGATGCCTGCCAGGGTGATTCTGGGGGCCCCCTGGTGTGTGGGGGA  
 GTCTTCAAGGTCTGGTGTCTTGGGGGTCTGTGGGGCCCTGTGGACAAGATGGCATCCCTGG  
 AGTCTACACCTATATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAACAAC**TGAC**  
 CTGTTTCTCCACCTCCACCCCAACCCCTTAACCTGGGTACCCCTCTGGCCCTCAGAGCACC  
 AATATCTCCTCCATCACTTCCCCTAGCTCCACTCTTGTGGCCTGGGAACTTCTTGGAACCTT  
 TAACTCCTGCCAGCCCTTCTAAGACCCACGAGCGGGGTGAGAGAAGTGTGCAATAGCTGGA  
 ATAAATATAAATGAAGGAGGGGCAAAAAAAAAAAAAA

**FIGURE 108**

MGLSIFLLLCVLGLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAH  
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLRLPVRVTSSV  
QPLPLPNDCATAGTECHVSGWGITNHPNPFDPDLQCLNLSIVSHATCHGVYPGRITSNMVC  
AGGVPGQDACQGDSGGPLVCGGVLQGLVSWGSGVPCGQDIPGVYTYICKYVDWIRMIMRNN

**Signal peptide:**

amino acids 1-17

108/249

**FIGURE 109**

GCGGCCACACGCAGCTAGCCGGAGCCCGGACCAGGCGCCTGTGCCTCCTCCTCGTCCCCTCGC  
 CGCGTCCGCGAAGCCTGGAGCCGGCGGGAGCCCCGCGCTCGCC**ATG**TCGGGCAGCTCAGCA  
 ACAGGTTCCAAGGAGGGAAGCGTTTCGGCTTGCTCAAAGCCCGGCAGGAGAGGAGGCTGGCC  
 GAGATCAACCGGGAGTTTCTGTGTGACCAGAAGTACAGTGATGAAGAGAACCCTCCAGAAAA  
 GCTCACAGCCTTCAAAGAGAAGTACATGGAGTTTGACCTGAACAATGAAGCGCAGATTGACC  
 TGATGCTCTTTAAAGAGGATGATGGAGAAGCTTGGTGTCCCCAAGACCCACCTGGAGATGAAG  
 AAGATGATCTCAGAGGTGACAGGAGGGGTGAGTGACACTATATCCTACCGAGACTTTGTGAA  
 CATGATGCTGGGGAAACGGTCGGCTGTCTCAAGTTAGTCATGATGTTTGAAGGAAAAGCCA  
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGAGACATTGCTAGCCTGCCCT**TGA**  
 GGACCCCGCCTGGACTCCCCAGCCTTCCCACCCCATACCTCCCTCCCGATCTTGCTGCCCTT  
 CTTGACACACTGTGATCTCTCTCTCTCATTGTGTTGGTCATTGAGGGTTTGTGTTGTTT  
 TCATCAATGTCTTTGTAAAGCACAAATTATCTGCCTTAAAGGGGCTCTGGGTGCGGGAATCC  
 TGAGCCTTGGGTCCCCTCCCTCTCTTCTTCCCTCCTTCCCGCTCCCTGTGCAGAAGGGCTG  
 ATATCAAACCAAAACTAGAGGGGGCAGGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC  
 CTCACTTGGAGGAACAGCACTCTCCATCCTTTCAGAAAGTCTCCAAGCCAAGTTCAAGGCTC  
 ACTGACCTGGCTCTGACGAGGACCCAGGCCACTCTGAGAAGACCTTGAGTAGGGACAAGG  
 CTGCAGGGCCTCTTTCGGGTTTCCTTGGACAGTGCCATGGTTCCAGTGCTCTGGTGTACCC  
 AGGACACAGCCACTCGGGGCCCCGCTGCCCCAGCTGATCCCCACTCATTCCACACCTCTTCT  
 CATCCTCAGTGATGTGAAGGTGGGAAGGAAAGGAGCTTGGCATTGGGAGCCCTTCAAGAAGG  
 TACCAGAAGGAACCTCCAGTCTGCTCTCTGCCCACACCTGTGCAGGCAGCTGAGAGGCAG  
 CGTGCAGCCCTACTGTCCCTTACTGGGGCAGCAGAGGGCTTCGGAGGCAGAAGTGAGGCCTG  
 GGGTTTGGGGGAAAGGTCAGCTCAGTGCTGTTCCACCTTTTAGGGAGGATACTGAGGGGAC  
 CAGGATGGGAGAAATGAGGAGTAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA  
 CTGAGAAATACAGGTTGCTTGCTGACCCCAATCTGCTTGAAAAA



**FIGURE 111A**

CGCGCTCCCCGCGCGCTCCTCGGGCTCCACGCGTCTTGCCCCGAGAGGCAGCCTCCTCCA  
 GGAGCGGGGCCCTGCACACATGCGCCCGGGTGGGCAGGGGTGGCGCCCGCGCTGCGCGCC  
 CGCTTGGCGCTGGCCTTGCGCGCTGGCGAGCGTCTTGAGTGGGCTCCAGCCCTCGCTTGGCC  
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGGCTGGGCTCCGCGCGGTTTC  
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATATCACCAGGATC  
 ACCAAGATTGGACTTCGCTGGGCTCAAGAACCTCCGAGTCTTGCATCTGGAAGACAACCAAGT  
 CAGCGTCATCGAGAGAGGCGCCTTCCAGGACCTGAAGCAGCTAGAGCAGCTGCGCCTGAACA  
 AGAATAAGCTGCAAGTCTTCCAGAATTGCTTTTCCAGAGCACGCCGAAGCTCACCAGACTA  
 GATTTGAGTGAAGAACAGATCCAGGGGATCCCGAGGAAGGCGTTCGCGCGCATCACCAGATGT  
 GAAGAACCTGCAACTGGACAACAACCATCAGCTGCATTGAAGATGGAGCCTTCCGAGCGC  
 TGCGCGATTGGAGATCCTTACCCTCAACAACAACATCAGTCGCGCATCCTGGTCACCAGC  
 TTCAACCACATGCCGAAGATCCGAACCTGCGCGCTCCACTCCAACCACCTCTACTGCGACTG  
 CCACCTGGCCTGGCTCTCGGATTGGCTGCGACAGCGACGGACAGTTGGCCAGTTACACACTCT  
 GCATGGCTCCTGTGCATTTGAGGGGCTTCAACGTGGCGGATGTGCAGAGAAGGAGTACGTG  
 TGCCCGAGCCCCCACTCGGAGCCCCCATCCTGCAATTGCCAACTCCATCTCCTGCCCTTCGCC  
 CTGCACTGCGAGCAATAACATCTGGACTGTGCGAGAAAGGGCTTGATGGAGATTCTCGCCA  
 ACTTGCCGGAGGGCATCTGCGAAATACGCTTAGAACAGAACTCCATCAAAGCCATCCCTGCA  
 GGAGCCTTCAACCCAGTACAAGAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA  
 TATTGCTCCAGATGCCTTCCAGGGCCTGAAATCACTCACTACATCGTGGCTGTATGGGAACA  
 AGATCACCAGATTGCCAAGGGACTGTTTGATGGGCTGGTGTCCCTACAGCTGCTCCTCCTC  
 AATGCCAACAAGATCAACTGCCTGCGGGTGAACACGTTTCAGGACCTGCAGAACCTCAACT  
 GCTCTCCCTGTATGACAACAAGCTGCGAGCCATCAGCAAGGGGCTCTTCGCCCTCTGCGAGT  
 CCATCCAGACACTCCACTTAGCCAAAACCACTTTGTGTGCGACTGCCACTTGAAGTGGGCTG  
 GCCGACTACCTCCAGGACAACCCCATCGAGACAAGCGGGGCCGCTGCAGCAGCCCGCGCGG  
 ACTCGCCAACAAGCGCATCAGCCAGATCAAGAGCAAGAAGTTCCGCTGCTCAGGCTCCGAGG  
 ATTACCGCAGCAGGTTTCCAGCAGCGAGTGTTCATGGACCTCGTGTGCCCGCAGAAAGTGTGCG  
 TGTGAGGGCACGATTGTGGACTGCTCCAACCAGAAGCTGGTCCGATCCCAAGCCACCTCCC  
 TGAATATGTACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTTGCA  
 TCTTCAAGAAGTTGCCCAACCTGCGGAAATAAATCTGAGTAACAATAAGATCAAGGAGGTG  
 CGAGAGGGAGCTTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACCACT  
 GGAGACCTGTCACGGGCGGTGTTCCTGGCCCTCAGTGGCCTCAAAACCTTGATGCTGAGGA  
 GTAACCTGATCAGCTGTGTGAGTAATGACACCTTTGCCGGCCTGAGTTCCGTTGAGACTGTGT  
 TCCCTCTATGACAATCGGATCACCACCATCACCCCTGGGGCCTTCAACACGCTTGTCTCCCT  
 GTCCACCATAAACCTCCTGTCCAACCCCTTCAACTGCAACTGCCACTGGCCCTGGCTCGGCA  
 AGTGGTTGAGGAAGGCGGATCGTCACTGGGAACCTCAGTGGCCAGAGGCCATTTTTCCTC  
 AAGGAGATTCCATCCAGGATGTGGCCATCCAGGACTTCACTGTGATGGCAACAGGAGAG  
 TAGCTGCCAGCTGAGCCCGGCTGCCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCAT  
 CGAGCAACAAGGGGCTCCGCGCCCTCCCGAGGGCATGCCAAGGATGTGACCCAGCTGTAC  
 CTGGAAGGAACCACTAAAGCCGTGCCAGAGAGCTGTCCGCCCTCCGACACCTTGACGCT  
 TATTGACCTGAGCAACAACAGCATCAGCATGCTGACCAATTACACCTTCACTAATATGTCTC  
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCGTCCACGCCTTCAAC  
 GGGCTGCGGTCCTGCGAGTGCTAACCCTCCATGGCAATTGACATTTCCAGCGGTTCCGTAAGG  
 CTCCTTCAACGACCTCACATCTTTCCCATCTGGCGCTGGGAACCAACCACTCCACTGTG  
 ACTGCACTTCTCGGTGGCTGTGCGAGTGGGTGAAGGCGGGGTACAAGGAGCCTGGCATGCC  
 CGCTGCACTAGCCCTGAGCCCATGGCTGACAGGCTCCTGCTCACCACCCCAACCCGCTT  
 CCAGTGCAAGGGGCAATGGACATCAACATTGTGGCCAATGCAATGCTGCCCTTCCAGCC  
 CGTGCAAGAATAACGGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCTTCCCC

**FIGURE 111B**

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA  
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTTTCAGCTGCTCCTGCCCTC  
 TGGGCTTTGAGGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCCGAA  
 AACAAATGCCACCTGCGCTGGACGGGATCAACAACCTACGTGTGTATCTGTCCGCCCTAACTACAC  
 AGGTGAGCTATGCGACGAGGTGATTGACCACCTGTGTGCCTGAGCTGAACCTCTGTGAGCATG  
 AGGCCAAGTGCAATCCCCCTGGACAAAGGATTTCAGCTGCGAGTGTGTCCCTGGGTACAGCGGG  
 AAGCTCTGTGTGAGCAGACAATGATGACTGTGTGGCCCAAGTGCCGCCACGGGGGCCAGTG  
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCCAGGGCTTCAGTGGACCCCTTCTGTG  
 AACACCCCCCACCATGGTCTCTACTGCAGACCAGCCCATGCGACCACTACGAGTGCCAGAAC  
 GGGGCCCAGTGTCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACACAGGCTTCGCCGG  
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAACTGG  
 CCTCCGCCAAGGTCCGACCCAGGCCAACATCTCCCTGCGAGGTGGCCACTGACAAGGACAAC  
 GGCATCCTTCTCTACAAGGAGACAATGACCCCTGGCACTGGAGCTGTACCAGGGCCACGT  
 GCGGCTGGTCTATGACAGCCTGAGTTCCTCCCAACCACAGTGTACAGTGTGGAGACAGTGA  
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAGTAGTG  
 GACAAAGGAACTCCAAGAGCCTGGGGAAGCTCCAGAAGCAGCCAGCAGTGGGCATCAACAG  
 CCCCCCTCTACCTTGGAGGCATCCCCACCTCCACCGGCTCTCCGCCCTTGCAGGACGACGG  
 ACCGGCTCTAGGCGGCTTCCACGGATGCATCCATGAGGTGCGCATCAACAACGAGCTGCGAG  
 GACTTCAAGGCCCTCCACACAGTCCCTGGGGGTGTACCAGGCTGCAAGTCTTGACCCGT  
 GTGCAAGCAGCGCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGCCGCCAG  
 GCTGGACCGGCCACTCTGCGACCAGGAGGCCCGGGACCCCTGCCTCGGCCACAGATGCCAC  
 CATGGAATAATGTGTGGCAACTGGGACCTCATACATGTGCAAGTGTGCCGAGGGCTATGGAGG  
 GGACTTGTGTGACAACAAGAAATGACTCTGCCAATGCCTGCTCAGCCTTCAAGTGTCAACATG  
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGCCCGGCTTTAGCGGC  
 GAGCACTGCCAACAAGAGAATCCGTGCCTGGGACAAGTAGTCCGAGAGGTGATCCGCCGCCA  
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCCATCATGGAATGTGCTGGGGGCT  
 GTGGGCCCCAGTGCTGCCAGGCCACCCGCAGCAAGCGGCGGAAATACGTCTTCCAGTGACAG  
 GACGCTCCTCGTTTGTAGAAGAGGTGGAGAGACACTTAGAGTGGCGCTGCCTCGCGTGTTC  
CTAAGCCCCCTGCCCGCTGCCTGCCACCTCTCGGACTCCAGCTTGATGGAGTTGGGACAGCC  
 ATGTGGGACCCCTGGTGATTACGATGAAGGAAATGAAGCTGGAGAGGAAGGTAAAGAGA  
 AGAGAAATATTAAGTATATTGTAAATAAACAACAAAAATAGAACTTAAAAAAAAAAAAAAAAA  
 AAAAAA



**FIGURE 112**

MAPGWAGVGA AVRARLALALASVLSGPPAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN  
 AERLDLDRNNITRITKMFAGLKNLRVLHLEDNQVSVIERGAFQDLKQLERLRNKNKLQVL  
 PELLFQSTPKLTRDLSENQIQGIPRKAFRGITDVKNLQLDNNHISCI EDGAFRALRDLEIL  
 TLNNNNISIRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVGQFTLCMAPVHL  
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV  
 EIRLEQNSIKAI PAGAFQYKKLKRIDISKQISDIAPDAFQGLKSLTSLVLVYGNKITEIAK  
 GLFDGLVSLQLLLLNANKINCLRVNTFQDLQNLNLLSLYDNKLQTISKGLFAPLQSIQTLHL  
 AQNPFFVDCDLKWLADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS  
 SECFMDLVCPEKCRCEGTIVDCSNQKLVRI PSHLPEYVTDLRNDNEVSVLEATGIFKKLPN  
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGNQLETVHGRVFRGLSGLKTMLLRSNLISCV  
 SNTDFAGLSSVRLLSLYDNRI TTTITPGAFTTLVSLSTINLLSNPFNCNCHLAWLGKWLKRKR  
 IVSGNPRCQKPFFLKEIPIQDVAIQDFTCDGNESSCQLSPRCPEQCTCMETVVRCSNKGRL  
 ALPRGMPKDVTLEYLEGNHLTAVPRELSALRHLTLDLSNNSISMLTNYTFSNMSHLSTLIL  
 SYNRLRCIPVHAFNGLRSLRVLT LHGNDISSVPEGSFNDLTSLSHLALGTNPLHCDCLRWL  
 SEWVKAGYKEPGIARCSSPEPMADRLLLLTPTHRFQCKGPVDINIVAKNACLSSPCKNNGT  
 CTQDPVELYRCACPYSYKGKDVPTINTCIQNPCQHGGTCHLSDSHKDGFS CSCPLGFEGQR  
 CEINPDDCEDNDCENNA TCVDGINNYVCICPPNYTGELCDEVIDHCVP ELNLCQHEAKCIP L  
 DKGFSCCEVPGYSGKL CETDNDDCAHKCRHGAQCVD TINGYTCTCPQGFSGPFCEHPPPMV  
 LLQTSPCDQYECQNGAQCI VVQQEPTCRCP PGFAGPRCEKLITVNFVGKDSYVELASAKVRP  
 QANISLQVATDKDNGILLYKGDNDPLALELYQGHVRLVYDSLSPPTTVYSVETVNDGQFHS  
 VELVTLNQTLNLVVDKGT PKSLGKLQKQPAVGINSPLYLGGIPTSTGLSALRQGTDRPLGGF  
 HGCIEHRVINNELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVVCECRPGWTGPLC  
 DQEARDPCLGHRCHHGKCVATGTSYMCKCAEYGGDLCDKNDSANACSAFKCHHGQCHISD  
 QGEPYCLCQPGFSGEHCQQENPCLGQVVREVI RQKGYASCATASKVPIMECRGGCGPQCCQ  
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

**Signal peptide:**

amino acids 1-27

**FIGURE 113**

GGATGCAGGACGCTCCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTTCTTCCGCA  
 GACTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTTCAGTTCTGTCT  
 CCGGCAGGCTTTGAGG**ATGA**AGGCTGCGGGCATTCTGACCCTCATTGGCTGCCTGGTCACAG  
 GCGCCGAGTCCAAAATCTACACTCGTTGCAAACTGGCAAAAATATTCTCGAGGGCTGGCCTG  
 GACAATTACTGGGGCTTCAGCCTTGGAAGCTGGATCTGCATGGCATATTATGAGAGCGGCTA  
 CAACACCACAGCCCCGACGGTCTGGATGACGGCAGCATCGACTATGGCATCTTCCAGATCA  
 ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAACCACTGCCATGTCGCCTGC  
 TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAAATTGTTAAAGA  
 GACACAAGGAATGAACATATTGGCAAGGCTGGAAGAAAACATTGTGAGGGCAGAGACCTGTCCG  
 AGTGGA AAAAAGGCTGTGAGGTTTCC**TAA**ACTGGAAC TGACCCAGGATGCTTTGCAGCAAC  
 GCCCTAGGATTTGCAGTGAATGTCCAAATGCCTGTGTCATCTTGTCCTGTTTCCCTCCAATA  
 TTCCTTCTCAAAC TTGAGAGGGGAAAAATTAAGCTATACTTTTAAGAAAAATAAATAATTCCÀT  
 TTAAATGTC

**FIGURE 114**

MKAAGILTLIGCLVTGAESKIYTRCKLAKIFSRAGLDNYWGFSLGNWICMAYYESGYNTTAP  
 TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSALITDDLTDALICARKIVKETQGMN  
 YWQGWKKHCEGRDLEWKKGCEVS

**Signal peptide:**

amino acids 1-19

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**FIGURE 115**

CAGGCCATTTGCATCCCAGTCTCCTTGTGTTCCGAGCCAGGCCACACCGTCTCAGCAGTGT  
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCCTATTAAACTTGTACATGGCTCCC  
 CATTGGTTTTTTGGAGAAAAGTTCAAGCTTTTTACCTTGGTGTCTGCCTGTATCCAGTGTTT  
 AGGCTGGCTAGACGGCGGAAGAAGATCCTATTTTACTGTCACTTCCCAGATCTGCTTCTCAC  
 CAAGAGAGATTCTTTTCTTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA  
 CCACAGGCATGGCAGACTGCATCTTAGTCAACAGCCAGTTTACAGCTGCTGTTTTTAAGGAA  
 ACATTCAGTCCCTGTCTCACATAGACCTGATGTCTCTATCCATCTCTAAATGTACCAG  
 CTTTGACTCAGTTGTTCTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCCTGC  
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA  
 CAGCTGCGTGGAAGATTGACATCCCAAGATTGGGAGAGGGTTTATCTGATCGTGGCAGGTGG  
 TTATGACGAGAGAGTCTGGGAGATGTGGAACATTATCAGGAATTGAAGAAAAATGGTCCAAC  
 AGTCCGACCTTGCCAGTATGTGACCTTCTTGAGGTCTTTCTCAGACAAACAGAAAATCTCC  
 CTCTCCACAGCTGCACGTGTGTGCTTTACACCCAAGCAATGAGCATTGGCATTGTCCC  
 TCTGGAAGCCATGTACATGCAGTGCCAGTCATTGCTGTTAATTCGGGTGGACCCTTGGAGT  
 CCATTGACCACAGTGTACAGGGTTTCTGTGTGAGCCTGACCCGGTGCCTTCTCAGAAGCA  
 ATAGAAAAGTTTATCCGTGAACCTTCCTTAAAGCCACCATTGGGCTGGCTGGAAGAGCCAG  
 AGTGAAGGAAAAATTTCCCCCTGAAGCATTACAGAACAGCTCTACCGATATGTACCAAAC  
 TGCTGGT**ATAA**TCAGATTGTTTTTAAGATCTCCATTAATGTCATTTTTATGGATTGTAGACC  
 CAGTTTTGAAACCAAAAAGAAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA  
 CTTGAGTCTTGAATGTGAGCCACTTTCCTATATACCACACCTCCCTGTCCACTTTTCAGAAA  
 AACCATGTCTTTTATGCTATAATCATTCCAAATTTTGCCAGTGTTAAGTTACAAATGTGGTG  
 TCATTCCATGTTTACGAGAGTATTTTAATTATATTTTCTCGGGATTATTGCTCTTCTGTCTA  
 TAAATTTTGAATGATACTGTGCCTTAATTGGTTTTTCATAGTTTAAAGTGTGTATCATTATCAA  
 AGTTGATTAATTTGGCTTCATAGTATAATGAGAGCAGGGCTATTGTAGTTCACAGATTCAT  
 CCACCGAAGTGTTCACTGTCTCTGTTAGGGAATTTTTGTTTGTCTGTCTTTGCCTGGATC  
 CATAGCGAGAGTGCTCTGTATTTTTTTAAGATAATTTGTATTTTGCACACTGAGATATAA  
 TAAAAGGTGTTTATCATAAAAA

MPLKLVLHGSPLVFGKFKLFTLVSAIPVFLARRRKKILFYCHFPDLLLTKRDSFLKRLY  
RAPIDWIEEYTTGMADCLLVNSQFTAAVFKETFKSLSHIDPDVLYPSLNVTSFDSVVEKLD  
DLVPKGKKFLLLSINRYERKKNLTLEALEALVQLRGLTSSQDWERVHLIVAGGYDERVLENVE  
HYQELKKMVQQSDLGQYVTFLRFSFDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCFV  
IAVNSGGPLESIDHVSVTGLCEPDPVHFSEAIEKFIREPSLKTAGLARARVKEKFSPEAF  
TEOLRYRYPVTKLLHV

Signal peptide:

amino acids 1-15

**FIGURE 117**

GACTACGCCGATCCGAGACGTGGCTCCCTGGGCGGCAGAACC**ATGT**TGGACTTCGCGATCTT  
 CGCCGTTACCTTCTTGCTGGCGTTGGTGGGAGCCGTGCTCTACCTCTATCCGGCTTCAGAC  
 AAGCTGCAGGAATTCAGGGATTACTCCAACGAAGAAAAAGATGGTAATCTTCAGATATT  
 GTGAATAGTGGAAAGTTTGCATGAGTTCCTGGTTAATTTGCATGAGAGATATGGGCCCTGGGT  
 CTCTTCTGGTTTGGCAGGCGCCTCGTGGTTAGTTTGGGCACTGTTGATGACTGAAGCAGC  
 ATATCAATCCCAATAAGACATCGGACCCTTTTGAACCATGCTGAAGTCATTATTAAGGTAT  
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAAATGTATGAAAATGGTGT  
 GACTGATTCTCTGAAGAGTAACCTTGGCCCTCCTCCTAAAGCTTTCAGAAGAATTATTAGATA  
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCCCTCAGCCAGCATATGCTTGGTTTTGCT  
 ATGAAGTCTGTTTACACAGATGGTAATGGGTAGTACATTTGAAGATGATCAGGAAGTCATTCTG  
 CTTCAGAGAAGATCATGGCACAGTTTGGTCTGAGATTGGAAGGCTTCTAGATGGGTCAC  
 TTGATAAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT  
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTTCATTGACTC  
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG  
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGGCAATCTGTTTTTAAACCACCTCTGAA  
 GAAGTTCAAAAAAAATTATATGAAGAGATAAAACCAAGTTTTTGGAAATGGTCTGTACTCC  
 AGAGAAAATTGAGCAGCTCAGATATTGTGAGCATGTGCTTTGTGAAACTGTTGCAACTGCCA  
 AACTGACTCCAGTTTCTGCCAGCTTCAAGATATTGAAGGAAAAATTGACCGATTATTATT  
 CCTAGAGAGACCTCGTCCTTTATGCCCTTGGTGTGGTACTTCAGGATCCTAATACTTGGCC  
 ATCTCCACACAAGTTTGATCCAGATCGGTTTGATGATGAATTAGTAATGAAAACCTTTTCCT  
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTTGCATATATGGTGACCACA  
 GTACTTCTTAGTGATTGGTGAAGAGACTGCACCTACTTTCTGTGGAGGGACAGGTTATTGA  
 AACAAAGTATGAAGTGGTAACATCATCAAGGGAAGAAGCTTGGATCACTGTCTCAAAGAGAT  
 AT**TAAA**ATTTTATACATTTAAATCATTTGTTAAATTGATTGAGGAAAAACACCATTTAAAAA  
 AAATCTATGTTGAATCCTTTTATAAACAGTATCACTTTGTAATATAAACACCTATTTGTAC  
 TTAA

**FIGURE 118**

MLDFAIFAVTFLALVGAVLYLYPASRQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLH  
ERYGPFVVSFWFGRRLVSVLGTVDVLKQHINPNKTSDPFETMLKSLLRYSQGGGSVSENHMRK  
KLYENGVTDSLKSNFALLLLKSEELLDKWLSTYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE  
DDQEVIRFQKNHGTWVSEIGKGFLDGS�DKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS  
QHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTWAICFLTTSSEEVQKKLYEEINQVF  
GNGPVTPEKIEQLRYCQHVLCEVVRTAKLTPVSAQLQDIEGKIDRFIIIPRETLLVLYALGVVL  
QDPNTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQCEPELRFAYMVTTVLLSVLVKRLHLLS  
VEGQVIETKYELVTSSREEAWITVSKRY

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 271-290

**FIGURE 119**

CTAGATTTGTCGGCTTGCGGGGAGACTTCAGGAGTCGCTGTCTCTGAACCTCCAGCCTCAGA  
GACCGCCGCCCTTGTCCCCGAGGGCC**ATG**GGCCGGGTCTCAGGGCTTGTGCCCTCTCGCTTC  
CTGACGCTCCTGGCGCATCTGGTGGTCGTCATCACCTTATTCTGGTCCCGGGACAGCAACAT  
ACAGGCCTGCCCTGCCCTCTCACGTTACCCCCGAGGAGTATGACAAGCAGGACATTACAGCTGG  
TGGCCGCGCTCTCTGTACCCCTGGGCCTCTTTGCAGTGGAGCTGGCCGGTTTCCTCTCAGGA  
GTCTCCATGTTCAACAGCACCCAGAGCCTCATCTCCATTGGGGCTCACTGTAGTGCATCCGT  
GGCCCTGTCCTTCTTCATATTCGAGCGTTGGGAGTGCACCTACGTATTGGTACATTTTGTCT  
TCTGCAGTGCCCTTCCAGCTGTCACTGAAATGGCTTTATTTCGTACCCGTCTTTGGGCTGAAA  
AAGAAACCTTCT**CA**ATTACCTTCATGACGGGAACCTAAGGACGAAGCCTACAGGGGCAAGGG  
CCGCTTCGTATTCTTGAAGAAGGAAGGCATAGGCTTCGGTTTTCCCTCGGAAACTGCTTC  
TGCTGGAGGATATGTGTTGGAATAATTACGTCTTGAGTCTGGGATTATCCGCATTGTATTTA  
GTGCTTTGTAATAAAATATGTTTTGTAGTAACATTAAGACTTATATACAGTTTtaggggaca  
ATTAAAAAAAAAAAAA



amino acids 12-28 (type II), 51-66, 107-124

**FIGURE 121**

TCCCGGACCCTGCCGCCCTGCCACTATGTCCC GCCGCTCTATGCTGCTTGCCTGGGCTCTCC  
 CCAGCCTCCTTCGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA  
 GTGCCCCGGAACGAGTGGAAGGCCCTGGCATCAGAGTGCGCCAGCACCTGAGCCTGCCCTT  
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCGCCTCGTGCCAGC  
 AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGGCTAC  
 AACTTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACCTCACGGGTGC  
 CCACTCAGGTCACCTTATGGAACCCCATGTCCATTGGCATCAGCTTCATGGGCAACTACATGG  
 ATCGGGTGCCACACCCAGGCCATCCGGGCAGCCCAGGGTCTACTGGCCTGCGGTGTGGCT  
 CAGGGAGCCCTGAGGTCCAACATATGTGCTCAAAGGACACCGGGATGTGCAGCGTACACTCTC  
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCCCTGAGGCC  
 CTGCTGATCCGCACCCCATTCCTCCCTCCCATGGCCAAAAACCCACTGTCTCCTTCTCCA  
 ATAAAGATGTAGCTC

**FIGURE 122**

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSFGNQLYHL  
IQNWPHYRSP

**Signal peptide:**

amino acids 1-20

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT  
AGSSCNTPASCQQQARNVQHYHMKTLGWCDVGYNFLIGEDGLVYEGRGWNFTGAHSGHLWNP  
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSFGNQLYHL  
IQNWPHYRSP

**FIGURE 123**

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAGGAAG**ATG**CAACT  
 GACTCGTGCTGCTTCGTGTTCTCGTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG  
 ATGATGGTCTCCCGGCTCAGAGGACCCCTGAGCGTGATGACCACGAGGGCCAGCCCCGGCCC  
 CGGGTGCCCTCGGAAGCGGGGCCACATCTCACCTAAGTCCCGCCCCATGGCCAATTCCACTCT  
 CCTAGGGTGCTGGCCCCGCTGGGGAGGCTTGGGCATTCTTGGGCAGCCCCCAACCGCC  
 CGAACCACAGCCCCCACCCTCAGCCAAGGTGAAGAAATCTTTGGCTGGGGCGACTTCTAC  
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGGAAGATTGTGGACCATGGCAA  
 TGGGACCTTCAGCGTCCACTTCCAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC  
 TCGTGCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG  
 GCCTCCAAAATCTTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGGCCCGCGGACCTC  
 GCTTTGCACCCACGACCCAGCCAAGATCTGCTCCCGAGACCACGCTCAGAGCTCAGCCACCT  
 GGAGCTGCTCCAGGCCCTTCAAAGTCGTCTGTGTCTACATCGCCTTCTACAGCACGGACTAT  
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGATACCCCTACTACCCATC  
 TGGG**TGA**CCCCGGGCGAGGCCACAGAGGCCAGGCCAGGGCTGGAAGGACAGGCCTGCCCATGC  
 AGGAGACCATCTGGACACCGGCGAGGGAAGGGGTTGGGCCTCAGGCAGGGAGGGGGGTGGAG  
 ACGAGGAGATGCCAAGTGGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCCAAGTG  
 CTGGTCCCAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGAGTGGGCT  
 CTCTGTGCAGCCTCACAGGGCTTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC  
 TGTGGGCGAGCCGATCAGTGTGGCCCAGATCAAGTCATGGGAGGAAGCTAAGCCCTTGGTT  
 CTTGCCATCTTGAGGAAAGATAGCAACAGGGAGGGGGAGATTTCATCAGTGTGGACAGCCTG  
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCTTAGGAGCCAGTCAGCAGGGTGGGGTGGGC  
 CAGAGGAGCTCTCCAGCCCTGCCTAGTGGGCGCCCTGAGCCCTTGTCTGTGCTGAGCATG  
 GCATGAGGCTGAAGTGGCAACCTGGGGTCTTTGATGTCTTGACAGATTGACCATCTGTCTC  
 CAGCCAGGGCACCCCTTTCCAAAATTCCCTCTTCTGCCAGTACTCCCCCTGTACCACCCATT  
 GCTGATGGCACACCCATCCTTAAGCTAAGACAGGACGATTGTGGTCTCCACACTAAGGCC  
 ACAGCCCATCCGCGTGCTGTGTGTCCTCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG  
 CATCCATGTCCGGAGAGGGGTCCCTCAACAGTCAGCCTCACCTGTCAGACCGGGGTCTCC  
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGCGGGCACGGTGGGGCGGGGCCGGCCGCAGA  
 GCATGTCTGGATCTGTTCTGTGTGTCTGTCTGTGGTGGGGGAGGGGAGGGAAGTCTTGT  
 GAAACCGCTGATTGCTGACTTTTGTGTGAAGAATCGTGTTCTTGAGACAGGAAATAAGCCTT  
 GCCCCGGGGCA

**FIGURE 124**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521  
><subunit 1 of 1, 252 aa, 1 stop  
><MW: 28127, pI: 8.91, NX(S/T): 5  
MQLTRCCFVFLVQGSPLYVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN  
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYFYSNIKTVALNLLVTGKIVD  
HGNGTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIEAKASKIFNCRMEWEKVERGR  
RTSLCTHDPKICSRDHAQSSATWSCSQPFKVVVCVYIAFYSTDYRLVQKVCPCDYNHSDTPY  
YPSG

**Important features of the protein:****Signal peptide:**

amino acids 1-14

**N-glycosylation sites.**

amino acids 62-65, 127-130, 137-140, 143-146

**2-oxo acid dehydrogenases acyltransferase**

amino acids 61-71

**FIGURE 125**

GTGAATGTGAGGGTTTGATGACTTTTCAGATGTCTAGGAACAGAGTGGGTGCAGGGGCCCA  
GGCAGGGCTGATTCTTGGGCGGAGGAGAGTAGGGTAAAGGGTTCTGCATGAGCTCCTTAAAG  
GACAAAGGTAACAGAGCCAGCGAGAGAGTCTGAGGGGAGACTTTGACTTCAAGCCACAGAAT  
TGGTGAAGTGTGCGCGCCGCCGCGCTCGTCCCTGCAGCGCTGTCGACCTAGCCGCTAG  
CATCTTCCCAGACCCGGATCCCGGGTAGGAGGCGACGCGGGCGAGACCAGCGCCAGCC  
GGCTGCGGCTGCCACACGGCTCACCATGGGCTCCGGGCGCGGGCGCTGTCCGCGGTGCCG  
GCCGTGCTGCTGGTCCTCACGCTGCCGGGGCTGCCCGTCTGGGCACAGAACGACACGGAGCC  
CATCGTGCTGGAGGGCAAGTGCTGCTGGTGGTGTGCGACTCGAACCCGGCCACGGACTCCAAGG  
GCTCCTCTTCTCCCCGCTGGGGATATCGGTCCGGGCGGCCAACTCCAAGGTGCGCTTCTCG  
GCGGTGCGGAGCACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTTACTT  
CGATCAGATCCTGGTGAATGTGGGTAATTTTTTACATTGGAGTCTGTCTTTGTAGACCAA  
GAAAAGGAATTTACAGTTTCAGTTTTCACGTGATTAAAGTCTACCAGAGCCAACTATCCAG  
GTTAACTTGTATGTTAAATGGAACACAGTAATATCTGCGCTTTCGCGGGGACAAAGATGTTAC  
TCGTGAAGCTGCCACGAATGGTGTCTGTCTACCTAGATAAAGAGGATAAGGTTTTACCTAA  
AACTGGAGAAAGTAATTTGGTTGGAGGCTGGCAGTATTCACGTTTTCTGGCTTTCTGGTG  
TTCCCCCTATAGGATTCAATTTCTCCATGATGTTTCATCCAGGTGAGGGATGACCCACTCCTG  
AGTTATTGAAGATCATTTTTTTCATCATTGGATTGATGTCTTTTATTGGTTTCTCATGGGTG  
GATATGGATTCTAAGGATTTCTAGCCTGTCTGAACCAATACAAAATTTACAGATTATTTGTG  
TGTGTCTGTTTCAGTATATTTGGATTGGGACTCTAAGCAGATAATACCTATGCTTAAATGTA  
ACAGTCAAAAGCTGTCTGCAAGACTTATTTCTGAATTTTCATTTCTGGGATTACTGAATTAGT  
TACAGATGTGGAATTTTATTGTTTAGTTTTTAAAGACTGGCAACCAGGTCTAAGGATTAGA  
AAACTCTAAAGTTCTGACTTCAATCAACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG  
TGTTAATATATTGATTATATTTGTTTTTATTCCTTTGGAATTAGTTTGTGTTGTTCTGTAA  
AAAACCTGGATTTTTTTTTTTCAGTAACGGTATTATGTTTTCTCTTAAAAAAGGTAATGAA  
TGGCTTGCCACAAATTTACCTTGACTACGATATCATCGACATGACTTCTCTCAAAAAAA  
GAATGCTTCATAGTTGTATTTTAAATGTATATGTGAAGAGTCATATTTTCCAAGTTATATT  
TTCTAAGAAGAAGATAGATCATAAATCTGACAAGGAAAAAGTTGCTTACCCAAAATCTAAG  
TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCTCCGAGGGAATCTTATACTTTTATTGC  
TCAACTTTAATTAATGATTGATAATAACCACTTTATTA AAAACCTAAGGTTTTTTTTTT  
TCCGTAGACATGACCACTTTATTAACCTGGTGGTGGGATGCTGTTGTTTCTAATTATACCTAT  
TTTTCAAGGCTTCTGTTGTATTTGAAGTATCATCTGGTTTTGCCTTAACCTCTTTAAATTTGA  
TATATTTATCTGTTTAGCTAATATTAATTCAAATATCCCATATCTAAATTTAGTGAATAT  
CTTGCTTTTGTATAGGTCATATGAATTCATAAAATTATTTATGTCTGTTATAGAATAAGA  
TTAATATATGTTAAAAAA

**FIGURE 126**

MSGRRALSAPPAVLLVLTLPGLPVWAQNDTEPIVLEGKCLVVCDSNPATDSKGSSSSPLGI  
 SVRAANSKVAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNFFTLESVFVAPRKGISFSF  
 HVIKVIYQSQTIQVNLMLNGKPVISAFAGDKDVTREATNGVLLYLDKEDKVYLKLEKGNLVG  
 GWQYSTFSGFLVFPL

**Signal peptide:**

amino acids 1-27

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**FIGURE 127**

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTTCGGCTGCGCCTTCATTGCCTTCGGGCCTGCGCTC  
GCCCTTTATGTCTTCACCATCGCCATCGAGCCGTTGCGTATCATCTTCTCATCGCCGGAGC  
TTTCTTCTGGTTGGTGTCTCTACTGATTTTCGTCCCTTGTTTGGTTCATGGCAAGAGTCATTA  
TTGACAACAAAGATGGACCAACAGAAATATCTGCTGATCTTTGGAGCGTTTGTCTCTGTC  
TATATCCAAGAAATGTTCCGATTTGCATATTATAAACTCTTAAAAAAGCCAGTGAAGGTTT  
GAAGAGTATAAACCCAGGTGAGACAGCACCCCTCTATGCGACTGCTGGCCTATGTTTCTGGCT  
TGGGCTTTGGAATCATGAGTGGAGTATTTTCCTTTGTGAATACCCCTATCTGACTCCTTGGG  
CCAGGCACAGTGGGCATTTCATGGAGATTCTCCTCAATTCTTCCTTTATTCAGCTTTTCATGAC  
GCTGGTCATTATCTTGCTGCATGTATTCTGGGGCATTGTATTTTTTGATGGCTGTGAGAAGA  
AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTGAGCCAGACCTTC  
ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTCTATGGGCAC  
CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTCTGCCAAG  
ACAAGAACTTCTTCTTTACAACCAGCGCTCCAGAT**TAA**CTCAGGGAACCAGCACTTCCCAA  
ACCGCAGACTACATCTTTAGAGGAAGCACAACTGTGCCTTTTTCTGAAAATCCCTTTTCTG  
GTGGAATTGAGAAAGAAATAAACTATGCAGATA



**FIGURE 128**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658  
><subunit 1 of 1, 257 aa, 1 stop  
><MW: 28472, pI: 9.33, NX(S/T): 0  
MTAAVFFGCAFTAFGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN  
KDGPTQKYLLIFGAFVSUYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF  
GIMSGVFSFVNTLSDSLPGTVGIHGDS PQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKW  
GILLIVLLTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRSCLKCLLCQDKN  
FLLYNQSR

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domains:**

amino acids 32-51, 119-138, 152-169, 216-235

**Glycosaminoglycan attachment site.**

amino acids 120-123

**Sodium:neurotransmitter symporter family protein**

amino acids 31-65

# FIGURE 129

CGGCAACACGCGCGCCGCCACCCGCTGCCACTGCCGCCCTGCCGGGGCCATGTTCCCTCTGGGCTTGCCTTCTT  
TGGTGCTCTTGGTGGCTCGGTGCAGAGGCCATCTGGGGGTTCTGGGGCCCAAGAACGCTCTGCAGAAAGACGCCG  
AGTTTGGAGCCACTAGCTGGACAGGTCAACAGCGAGCTGGTCAACATCTACACCTCTCAACCTACTGTGACCC  
GCACAGGACAGAGGGCGCTGGCTGTGCTGTGAAGCTCTGAACAGCAGAGGGGGGCCGCTGTGCTTTTGTGG  
TCCGCCAGAGAGGGCTGTGGGTCTCCTTCCAGGTGCCCTAATCTCTGCGAGGGATGTTTACGGCCAAGTACCTCT  
ACCAAAAAGTGGAAACGAACCTGTGTGTCAGCCCCCACCACGAATGAGTCGGAGATTGAGTCTCTCTACGTGGATG  
TGTCCACCTGTCAACAGTCAACACACATACCAGCTCCGGGTACGCCGATGGACGATTTTGTGCTCAGGACTG  
GGGAGCAGTTGAGCTTCAATACACAGCAGCAGCAGCCAGTACTTCAAGTATGAGTTCCTGTAGGCGTGAGCT  
CGGTAAATGTCAAGGTGACCTCCAACAGGCCCTTCCCTGCTCAGTCATCTCCATCAGGATGTGCTGTCTCTG  
TCTATGACCTGGACAAACAGCTAGCCTTTCATCGGCATGTACACAGCATGACCAGAAAGCGGCCATCACCGTAC  
AGCGCAAAGACTTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTCGGGGGCT  
CCCTGCCCTTCTACCCCTTCGCAGAGATGATCCGGTGCATCAAGGCCACCGCCAGAAAACCTGTGAGTGTCTGG  
TGTCTCAAGCAGTCACTGTGAGGCATACGTGAGTGGGATGCTCTTTGCTGGGTATATTTCTCTCCTTTTAC  
TGTGACCGTCTCTCTGGCTGCTGGGAGAACTGGAGGCAGAGAAGAACCTGCTGTTGCCATTGACCGAG  
CTGCCCCAGAAAGCGGTACCTCTGAGTCTGGGTGATTCTTTCTGGCAGTTCCCTTATGAGGGTTACAACT  
ATGGCTCCTTTGAGAATGTTTCTGGATCTACCGATGGTCTGTTGACAGCGCTGGCATTGGGGACCTCTCTTACG  
GTTACACGGGCCGCTCCTTTGAACTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGAGGATG  
ACTACGACATCTGACCGCATCGATTCCGCAAGAATGTCACTTCCGACCAAGAACTACCTCTATGTGGCTGAC  
TGGCGGCAAGGACAGCGGTGTTCTGCGGAAAAAGTACCAGTCTACTCTTGGAACTTGGCCACTGTGCTCT  
TCTATGCCCTTCTGTGGTGCAGCTGGTGAATCACTACCAGACGGTGGTGAATGACAGGAATGACAGCATCT  
GCTACTACAACTCTCTGCTCGCCACCCACTGGGCAATCTCAGCGCTTCAACAACTCTGACAACTCGGGGT  
ACATCTGCTGGGGCTGCTTTTCTGTCTCATCATCTGCAACGGGAGATCAACCAACCGGGCCCTGCTGCGCA  
ATGACCTCTGTGGCTGGAATGTGGGATCCCAAACTCTTGGGCTTTTCTACCGCATGGGCAACGCCCTGATGA  
TGGAGGGGCTGCTCAGTGGCTTGTATCATGTGTGCCCAACTATACCAATTTCCAGTTTGACACATCGTTCTATGT  
ACATGATCGCGGACCTGTGATCGTGAAGCTCTACCCAGAGCGGACCCGAGCATCAAGCCACGCGCTACAGTG  
CCTACGCTCTCCTGGCCATTGCTCTTCTCTGTGCTGGGCGTGTCTTGGCAAAAGGAACACGGCGCTTCT  
GGATCGCTCTTCTCATCATTCATCATCTGCCACCTGCTCCTCAGCAGCGAGCTCATTTACATGGGCGGTGGGA  
AATGGACTCGGGGATCTTCCGCCATCCTCCAGTGCTCTACACAGACTGCATCCGGCAGTGCAGCGGGCCG  
TCTACGTGGACCGCATGTTGCTGCTGTGTCATGGGCAACGTCACTAAGTGGTGGTGGCTGCTATGGGCTTATCA  
TGCGCCCCAATGATTTCGCTTCTACTTTTGGCCATTGGCATCTGCAACCTGTGCTTTTACTTCGCTTCTACA  
TCATCATGAAGCTCCGGAGTGGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCACTGCTTTGACACTCOGTGGTCT  
GGGGCTTCGCGCTCTTCTTCTTCTCCAGGACTCAGCACTGGCAGAAAACCTGCAAGATCGAGGGAGGACCA  
ACCGGGACTGCATCCTCTCGACTTCTTTGACGACCAAGCATCTGGCACTTCTCTCTCTCATCGCATGTTCG  
GGTCTCTCTGCTGTGACACTGGATGACGACTGGATCTGTGACGGGCAAGATCATGTCTTCTAGC  
AGGAGCTGGGCGCTTCGCTTCACCTCAAGGGGCGCTGAGTCTCTTGTGTCATAGACCGGTCACTCTGTCTGTG  
TGGGGATGAGTCCCAGCCAGCGCTGCCAGCACTGGATGGCAGCAGGACCGAGTCTAGGCTTGGCTTGGCT  
GGGACGCCATGGGTGGCATGGAACCTTGCAGCTGCCCTTCCGAGGAGGACAGGCTCTCCTCCCTGGAACCCCC  
AGATGTTGGCCAAATGCTGCTTCTCTCAGTGTGGGGCTTCCATGGGCGCTGCTCTTGGCTCTCATT  
TGCTCCTTCAAGAGGAAGGATGGAAGGACACCTTCCCAATTCATGCCTTGCATTTTGGCGCTCTCTCTCCCC  
ACAATGCCCGACCTGGGACCTTGAAGCCCTCTTTTCTCCCACTACTCCCACTCAGGGGCTAGTCTGGGGCTGA  
ATCTCTGCTGCTGATCAGGGCCCCAGTCTCTCTTGGGCTGTCCCTGGCTGCCATCACTGCCCATTCAGTCAAGC  
AGGATGGATGGGGTATGAGATTTTGGGGGTGGCCAGCTGGTGCCAGACTTGTGGTCTAAGGCGTGAAGGGG  
CTGGGGCAGTGCGTATTTCTTCTCCTCTGACCTGTGCTCAGGGCTGGCTCTTTAGCAATGCGCTCAGGCCAAT  
TGGAAACCGCTTCTGATTCAAGAGGCTGAATTCAGAGGTCACTCTTCACTCAGCTCCAGACTCCAGACTGAGC  
AGCACCAGACTGGAGGAGGAGCGGCTTACCCCTTCCCTTCTCTTCCAGGCGCTTAGTCTTGCACCAACCC  
AGTGTGTGGCTTTTCAGTGCAATGACACTGCCCCAAGATGTCCAGGGGCAAGGAGGAGGATTCAG  
CCGCTTCTGCTCTCAGACTGTGGGCACCCAGTGCTTACCTTAGAAGGGGCTTCAGGAAGGATGTGCTGTTT  
CCCTTACGTGCCCACTCTAGCCTCGCTTAGGACAGGGCTGGCTCTTAAGTTTTCGTCAGCTCTTCAGGCA  
AGTTCTGCTGTAGTCTGACACACATACCTATGAACCTTGGAGTTTACAAAGAAATGCCCGAGCTTGGGCA  
CTGGCCACCTGCTGCTTGGATCCCTTCTGCTCCACTGCTCACCCGAGTCTGAGGATGGGGAGCTCAGG  
CGGAGCCTCTGCTTTGGGATGGGATGTGTTTCTCCCAAACTGTTTTCATAGCTCTGCTTGAAGGGCTGGG  
AGGAGCTGGCTGTGATCTTTCTCAGAGGCTCTCCATGCTATGGTGCATTTCCGTTTCTATGAATGAAT  
TGCATTCATAAACAACAGCATCAAAAAA

**FIGURE 130**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNVLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKLYLQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTEGFSEFNTTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFFPCSVISIQDVLCPVYDLNNAVAFIGMYQMTTKAAITVQRKDFPSNSFYVTVV
VKTEDQACGGSPLFPYFFAEDEFPVDQGHRQKTLVLVLSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVLAIDRACPEGHPRVLADSFPGSSPYEGYNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSEFPGVTRPRVDSMSSVEEDDYDTLTDIDSDKNVIRTQYLYVADL
ARKDKRVLRRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVNTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIILQREINHNRRALLRNDLCALECGIPKHFGLEYAMGTALM
MEGLLSACYHVCNPYNTNFQFDTFSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVFFS
VLGVVFGKNTAFWIVFSIIHIIATLLLSQLYLYMGRWKLDSGIFRRILHVLVYTDICIRQCSG
PLYVDRMVLVLMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLLYFAFYIIMKLRSGERI
KLIPLLCIVCTSVVWGALFFFFQGLSTWQKTPAESREHNRDCILLDFDDHDIWHFLSSIA
MFGSFLVLLTLDLDDLDTVQRDKIYVF

```

**Important features of the protein:****Signal peptide:**

amino acids 1-18

**Transmembrane domains:**

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

**Leucine zipper pattern.**

amino acids 497-518

**N-glycosylation sites.**

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

[illegible]

**FIGURE 132**

MVPAWLWLLCVSPQALPKAQPaelSVEVPENYGGNFPLYLTKLPREGAEGQIVLSGDSG  
 KATEGPFAMDPDSGFLLVTRALDREEQAeyQLQVTLEMQDGHVLWGPQPVLVHVKDENDQVP  
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQFSPDMFQLEPRL  
 GALALSPKGSTSLDHALERTYQLLVQVKMDGQASGHQATATVEVSIIESTWVSLLEPIHLAE  
 NLKVLYPHHMAQVHWSSGGDVHYHLESHPPGPFfeVNAEGNLYVTRELDREAQAeyLLQVRAQN  
 SHGEDYAAPLELHVLVMDENDNVPICPPRDPTVSIPELSPPGTEVTRLsaEDADAPGSPNSH  
 VVYQLLSPEPEDGVEGRAfQVDPTSGSVTLGVLPraqNILLVLAMDLAGAEGGFSSTCE  
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTaIDADLEPAfRLMDFAIERGDTE  
 GTFGLDWEPDSGHVRLRLCKNLSYEAAPsHEVVVVVQSVAKLVGPGPGGATATVTVLVERV  
 MPPPKLDQESYEASVPISAPAGSFLlTIQPSDPISRTLRFSLVNDSEGWLCIEKFSGEVHTA  
 QSLQGAQPGDtyTVLVEAQDTALTlAPVPsQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF  
 TLGPNPTVQRDWRlQTLNGSHAYLTlALHWVEPREHIIPVVVSHNAQMWQLLVrVIVCRcNV  
 EGQCMRKVGRMKGMPTKLSAVGILVGTlVAIGIFlLILIFTHTWMSRKKDPDQPADSVPLKATV

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 762-784

**FIGURE 133**

CCGGGGACATGAGGTGGATACTGTTTCATTGGGGCCCTTATTGGGTCCAGCATCTGTGGCCAA  
 GAAAAATTTTTTGGGGACCAAGTTTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA  
 ATTGAGTCAACTAGTGAATTCAAACAACCTTGAAGCTCAATTTCTGGAAATCTCCCTCCTCCT  
 TCAATCGGCTGTGGATGTCCTGGTCCCATCTGTGTCAGTCTGCAGGCATTTAAATCCTTCCTG  
 AGATCCCAGGGCTTAGAGTACGCAGTGACAAATGAGGACCTGCAGGCCCTTTTAGACAATGA  
 AGATGATGAATGACAACAATGAAGGGCAAGAACCGAGCAGTAATAACTTCAACTACGGGG  
 CTTACCATTCCCTGGAAGCTATTACCACGAGATGGACAACATTCGCCGAGACTTTCTCGAC  
 CTGGCGAGGAGGGTGAAGATTGGACATTGCTTTGAAAACCGGCCGATGTATGTACTGAAGTT  
 CAGCACTGGGAAAGCGTGAGGCGGCCGCGCTTGGCTGAATGCAGGCATCCATTCCTCCGAG  
 AGTGGATCTCCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCGAGAG  
 GATCCAGCTATCACCTCCATCTTGGAGAAAATGGATATTTTCTTGTGTGCTGTGGCCAATCC  
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCGGTCCCGAAATC  
 CTGGAAGCTCCTGCATTGGTGTCTGACCCAAATAGAACTGGAAACGCTAGTTTTGCAGGAAAG  
 GGAGCCAGCGACAACCTTGTCTCCGAAGTGTACCATGGACCCACGCCAATTCGGAAGTGGAG  
 GGTGAATCAGTGGTAGATTTTCATCAAACACATGGGAATTTCAAGGGGCTTCATCGACCTGC  
 ACAGCTACTCGCAGCTGCTGTATCCATATGGGTACTCAGTCAAAAAGGCCCGCAGATGCC  
 GAGGAACCTGCACAAGGCTGGCGAGGCTTGCGCCCAAAGCTCTGGCTCTGTGTGCGCACTGA  
 GTACCAAGTGGGTCCCACTGCACTGTCTATCCAGCTAGCGGGAGCAGCATCGACTGGG  
 CGTATGACAACGGGCATCAAAATTTGCATTACATTTGAGATACCCGGAGACCTATGGC  
 TTCCTCCTGCCAGCTAACAGATCATCCCACTGCAGAGGAGACGTGGCTGGGGCTGAAGAC  
 CATCATGGAGCATGTGCCGGACAACCTCTACTAGCGCATGGCTCTGCTCTGTCTACATTTAT  
 TTGTACCCACACGTGCACGCACTGAGGCCATTGTTAAAGGAGCTCTTTCCTACTGTGTGAG  
 TCAGAGCCCTCTGGGTTTGTGGAGCACACAGGCCCTGCCCTCTCCAGCCAGCTCCCTGGAGT  
 CGTGTCTCTGGCGGTGTCCTGCAAGAACTGGTCTGCCAGCCTGCTCAATTTTGGTCTG  
 CTGTTTTTGTATGAGCCTTTTGTCTGTTCTCCTTCCAGCCTGTGGCTGGGCGGCTGCACCT  
 AGCATCACCCCTTCTGGGTGGCATGTCTCTCTACCTCATTTTTAGAACCAAGAACATC  
 TGAGATGATTTCTTACCCTCATCCACATCTAGCCAAGCCAGTGACCTTGCTCTGGTGGCACT  
 GTGGGAGACACCATTGTCTTTAGTGGGTCTCAAAGATGATGTAGAATTTCCCTTAAATTC  
 TCGCAGTCTTCTGGAAAATATTTTCTTTGAGCAGCAATCTGTAGGGATATCAGTGAAG  
 GTCTCTCCCTCCCTCCTCTCCTGTTTTTTTTTTTTTTTGGAGACAGATTTTGCTCTTGTGGC  
 CAGGCTGGAGTGTGATGGCTCGATCTTGGCTCACCACAACCTCTGCCTCTCGGGTCAAGCA  
 ATTCTCTGCCTCAGCCTTCTGAGTAGCTTGGTTTATAGCGCATGCCACCATGCTGGCTA  
 ATTTTGTGTTTTTGTAGTAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACCTCCCA  
 ACCTCAGGTGATCTGCCCTCCTTGGCCTCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG  
 TCGCGGCGCGTCCCTCCTTTTTTAGGCCTGAATCAAAAGTAGAAGATCACTTTCCCTCAC  
 TGTGCTGAGAATTTCTAGATACTACAGTTCTTACTCCTCTCTCCCTTTGTATTACGTGTG  
 ACCAGGATGGCGGGAGGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA  
 GTGACCATCTAAATTCAGGATGGTGAATATTACCCATCTGCTTAATGGGCTTACCTCCT  
 CTTTGGCTTTTGAATCACTCTCAAAGATCTAGGCCTCATCTTACAGGCTCAATACCTCAT  
 CTGGCTGGATATCTCACTGCCCTGGCACATTCCTATTGTGCTGTGGGTATCTGTGTT  
 TCCTTGTCTGTTTGT  
 TCTGTCTATTATTGTATCTGGACCACAAGTTTCTAAGTAGAGCAAGAATTCATCAACCACTG  
 GCCTCTGTTTTCATTTCCTCAGCAGTACCATCTGCTCTTGTGTGTGTGTGTGTGTGTGTGT  
 TGT  
 GCATCTGGTGTGTGCTTATAAGCCAATAAATATTCAATGTGAAAAAAAAAAAAAAAAAAAA

**FIGURE 134**

MRWILFIGALIGSSICGQEKFFGDQVLRINVRNGDEISKLSQLVNSNNLKLNFWKSPSSFN  
PVDVLVPSVSLQAFKSFLLRSQGLEAYVTIEDLQALLDNEDEMQHNEGQERSNNFNYGAYH  
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKGVRPAPVWLNAGIHSREWI  
SQATAIWTARKIVSDYQRDPATISILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS  
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDVFIQKHGNFKGFIDLHSY  
SQLLMYPYGYSVKKAPDAEELDKVARLAALKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD  
NGIKFAFTFELRDTGTYGFLLPANQIIPAEETWLGKTIMEHVRDNL

**Signal peptide:**

amino acids 1-16

CAACCATGCAAGGACAGGGCAGGAGAAGAGGAACCTGCAAGACATATTTTGTTCAAAATG  
GCATCTTACCTTTATGGAGTACTCTTTGCTGTTGGCCTCTGTGCTCCAATCTACTGTGTGC  
CCCGGCCAATGCCCCAGTGCATACCCCGCCCTTCCTCCACAAAGAGCACCCCTGCCTCAC  
AGGTGTATTCCCTCAACACCGACTTTGCCTTCCGCCTATACCGCAGGCTGTTTTTGGAGACC  
CCGAGTCAGAACATCTTCTTCTCCCTGTGAGTGCTCCACTTCCCTGGCCATGCTCTCCCT  
TGGGGCCCACTCAGTCACCAAGACCCAGATTCTCCAGGGCCTGGGCTTCAACCTCACACACA  
CACCAGAGTCTGCCATCCACCAGGGCTTCCAGCACCTGGTTCACTACTGACTGTTCCCAAGC  
AAAGACCTGACCTTGAAGATGGGAAGTGCCTCTTCGTCAAGAAGGAGCTGCAGCTGCAGGC  
AAATTTCTTGGGCAATGTCAAGAGGCTGTATGAAGCAGAAGTCTTTTCTACAGATTTCTCCA  
ACCCCTCCATTGCCCAGGCGAGGATCAACAGCCATGTGAAAAAGAAGACCAAGGGAAGGTT  
GTAGACATAATCCAAGGCTTGACCTTCTGACGGCCATGGTTCGTGTAATCACAATTTCTCT  
TAAAGCCAAGTGGGAGAAGCCCTTTCACCTTGATATACAGAAGAAGACTCCCATCTCTGG  
TGGGCAGCAGGTCAGTGTGCAGTCCCCATGATGCACAGAAGAGCAGTTCGCTTTTGGG  
GTGGATACAGAGCTGAAGTGCCTTTGTGCTGCAGATGGATTACAAGGAGATGCGGTGCGCTT  
CTTTGTCTCCCTAGCAAGGGCAAGATGAGGCAACTGGAACAGGCCTTGTGAGCCAGAACAC  
TGATAAAGTGGAGCCACTCACTCCAGAAAAGGTGGATAGAGGTGTTTCATCCCCAGATTTTCC  
ATTTCTGCCTCTACAATCTGGAACCACCTCTCCGAAGATGGGCATCCAAAATGCCTTTGA  
CAAAAATGCTGATTTTTCTGGAATTGCAAGAGAGACTCCCTGCAGGTTTCTAAGCAACCC  
ACAAGGCTGTGCTGGATGTCAGTGAAGAGGGCACTGAGGCCACAGCAGCTACCACCACCAAG  
TTCATAGTCCGATCGAAGGATGGTCCCTCTTACTTCACTGTCTCTCTCAATAGGACCTTCT  
GATGATGATTACAAATAAAGCCACAGACGGTATCTCTTTCTAGGGAAAGTGGAATAATCCCA  
CTAAATCCTAGTGGGAAATGGCCTGTTAACTGATGGGCACATTGCTAATGCACAAGAAATAA  
CAAACCACATCCCTCTTTCTGTTCTGAGGGTGCATTTGACCCCAAGTGAGGCTGGATTGCTG  
GCAGGGATGCCACTTCCAAGGCTCAATCACCACAAACCATCAACAGGGACCCAGTCACAAGCC  
AACACCCATTAAACCCAGTCACTGCCCTTTTCCACAAATTTCTCCAGGTAAGTAGCTTCATG  
GGATGTTGCTGGGTTACCATATTTCCATTCTTTGGGGCTCCAGGAATGGAATACGCCAAC  
CCAGGTTAGGCACCTCTATTGCGAATTACAATAACACATTCAATAAAACTAAAAATATGAAT  
TCAAAAAA  
AAAAAA



**FIGURE 136**

MASYLYGVLFVAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLE  
TPSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIIHQGFQHLVHSLTVP  
SKDLTLKMGSALFVKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQ GK  
VVDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF  
GVDTELNCFVLQMDYKGDVAFFVLPSKGMKRLQEQALSARTLIKWSHSLQKRWIEVFIPRF  
SISASYNLETILPKMGIQNAFDKNADFSGIKRDSLQVSKATHKAVLDVSEEGTEATAATTT  
KEIVRSKDGPSYFTVSFNRTFLMMITNKATDGIILFLGKVENPTKS

**Signal peptide:**

amino acids 1-20



**FIGURE 138**

MKMQKGNVLLMFGLLLHLEAATNSNETSTSTANTGSSVSSGASTATNSGSSVTSSGVSTATI  
SGSSVTSNGVSIVTNSEFHTTSSGISTATNSEFSTASSGISIATNSESSTSSGASTATNSE  
SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRASTATNSESSTLSSGASTATNSDSS  
TTSSGASTATNSESSTSSGASTATNSESSTVSSRASTATNSESSTSSGASTATNSESRTT  
SNGAGTATNSESSTSSGASTATNSDSSTVSSGASTATNSESSTSSGASTATNSESSTSS  
GASTATNSDSSTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATNSESSTSSGA  
NTATNSESSTVSSGASTATNSESSTSSGVSTATNSESSTSSGASTATNSDSSTTSSEAST  
ATNSESSTVSSGISTVTNSESSTSSGANTATNSGSSVTSAGSGTAALTGMHTTSHSASTAV  
SEAKPGGSLVPWEIFLITLVSVVAAGLFAGLFFCVRNSLSLRNTFNTAVYHPHGLNHGLGP  
GPGGNHGAPHRPRWSPNWFWRPVSIIAMEMSGRNSGP

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 510-532

**FIGURE 139**

GGGAGAGAGGATAAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTC  
 CCAGCAAT**ATG**CATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCC  
 CTGTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGG  
 GCTGAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGAATCACGC  
 ATGCCGGAAGGGAAGTGGAGAAGGTTTTCAACGGAAGTTCAGCAACATGGGGAGCCACACCGGC  
 AAGGAGTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGAT  
 CAACCATGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACG  
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCACACTGGGGTCCAC  
 CAGGCTGGGAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGG  
 AAAGGAAGTGGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC  
 TGCAGAATGCTCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGC  
 AACCATCAAAGCGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGG  
 GGCCTCAGTCAACACGCCTTTTCATCAACCTTCCCGCCTGTGGAGGAGCGTCGCCAACATCA  
 TGCCCT**TAA**ACTGGCATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTACATCAGCTGAC  
 ATGACCTGGAGGGGTTGGGGGTGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTG  
 GGATTTGTGAATAAACTTGATACACCA

**FIGURE 140**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAG
REVEKVFNGLSNMGSHTKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHVNNAAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPFINLPALWRSVANIMP
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Homologous region to circumsporozoite (CS) repeats:**

amino acids 35-225

CCCGGTTCCCGGAGGCTTCGCGCGGCGACCTTGGCAACGGGACAGTTCAGTGGACACTCAGGAAGAGGCGCG  
CCGCGGGGGGAGCTACAGCTGCGCTGACCTGACTACTCCAGGTCCGGAGCGGGGCCCCGGGGGAGCTCG  
GGGGCGGACCGCGGGGCGGAGCTGCCCGCTGATGTCGCGCGAGCCACTTGAGCCGCGAGCGCGGACACTCG  
CTCTCGTCTCTTCGGAATCTGCGACCGGATGGGGCTGAGGAGCTGGCTGCGGCCCATGGGGCGCGCTGCG  
CTCTGGCCACCGCTGCTGCTGCTCTGCTGCTCTGCTCTGCTGACGCCGCGCTCGACCTGGGGCGCTGACG  
CCCGGACTGAGCTGCTGCTGGCTCTCAGAGACGGCCATCTTCAGATTGCAAGTGAACACTTCTCAACTAC  
ACAGCCCTTCTGCTGAGCAGGGATGCGCAGGACCTTGCTACGTGGTGCTGAGAGGCGCTCTTTTGCACTCACTAGC  
CTCCTCAGCTTCTCTCGGAGCGGGATGATCAGGAGCTGCTTTGGGGTGCAGACGCGAGAAGAAACAGCACTGC  
AGCTTCAGGGCAGGAGCCACAGCGCGATGTGTCAAACTACATCAGATTCTCTCGCCCTCAGCGGCATCTC  
CTGTTCACCTCTGGGACAGCAGCTCTCAGCCCATGTGTACTCAATCAACATGAGNACTCACCTCGGACAA  
GACGAGAGGGGAATGTCTCTCGAAGATGGCAGGGCGGCTGTCTCCTTCGACCCAAATTTCAAGTCCACTGCC  
TGGTGTTGATGAGCGAGCTCTACACTGGAACTACACAGCAGCTTCAGAGGAATGACCGCGCATCTCGCGGCTG  
CAAAGCCTTCGCCCCAACAGACGAGAGCTCCCTCACTGGCTGGTCAAGACAGCCAGCTTTTGTGGCTCAGGCTAC  
ATTCTCGAGAGCGCTGGGAGCATTTGCAAGGCGATGATGACAGAACTTCACTTTTCTCAGGACAGCTGGCCAGAA  
TTTGAGTTCTTTGAGAAACAACTTTGTTCCGCAATTTCCGCGATCTGCAAGCTGAGGGTGAGAGAGCGGGT  
CTCAGCAGCGCGCTGGACCTTCTCTCAGGCCCGAGCTGTGTGCTCAGGCCGCGACGATGGCTTCCCTTCAACT  
GTGCTCGAGGATGTCTTACAGCTCAGGCCACGCCCGAGGATCGGTCGAGACACCTTTGCTTGGGTTCTTCACT  
TCCAGTGGGACAGGGGATACAGAGGCTCTCGCGCTCTGTGCTTTCACAATGAAGGATGTGCAGAGAGTCTCT  
AGCGGCTCTACAGAGGATGTGAACGTGAGACAGCAGTGGTACACGTGACCCCGGCGCCACACCCGGG  
CTCGAGGCTGCATCAACAACTGCCCCGGAAGAGGAATCAACTCATCCTCGACGCTCCAGACCGCGGTGCT  
AACTCTCTCAGGACCACTTCTGATGAGCGGCGAGTGGACGCGCATCTGCTGCTCGACCGCCAGGCTGCT  
TACCGGCTGCTGGCTGTACACGGCTCCCTGGCTCGGACCAACCTTACAGTCTCTCTCTCGGGACCTGTGTGA  
GAGCGGCTCCAAAGAGTACAGTGCAGTGGGCGGGGTGACATCATGAGGAGTGCAGATCTCTCATCGGGA  
CAGCCCGCTGCAAAATCTGTCTCGGACAGCCAGGGGGTGTCTGTATGGCGCTCACATCGGGGCTGATGCCA  
TGGCCATTTGGCCAACTCAGGCTCTATCCGAGTCTGGGGACGTGCTCTCGCGCGGGACCCCTATGTGCTGG  
CGCGCTCCAGCTGCGAAGCACTCAGCTCTACCCAGCTCAGTGGCCACAGGCGCTGGATCAGGACCTCAGG  
GGAGCCAGCGCGAAGACCTTTGACGCGGTCTTCGGTTGTGTCCGCTTTTGTATCAACGAGGAGGAAGCA  
TGTGAGCAAGTCTCAGTTTCAGGCCAACACAGTGAACACTTTGGCTCGGCCCTCTCTCAACCTGGGCGCGGA  
CTCTGGGTACGCAACGGGGCGCCGTCAATGCTGGCTCGCTGCAAGTGTACCACTCGGGACCTGTGTGCT  
GTGGGCAACCAACAGCTGGGGAGTTCCAGTCTGTGTCATAGGAGGGCTTCAGACAGCTGATAGGACGCTAC  
TGCCAGAGGTGTGTGAGAGCGGGTGGCGACAGCAACAGTAGAGGTGGCAGTGTACCGTATGATTACGACA  
TCGGTGTGATGTGCAACCACTGGTGGCAAGGACAGCTGGGGTGACAGACAGTCTCTACTGGAAGGATTCCTGT  
ATGTGCGAGCTCTTTTGTGCTGCGCTGCTGCTCCAGTTTATTATTCTGTCTACCGGCAAGGAACAGATGA  
GATCTCTTCAGAGCGGGGAATGTGCGAGCTGACCCCAAGACTGCCCTGGTGTGCTGCCCGCTGAGACCGCG  
CCACTCAACGCGCTTAGGGCCCCATAGACCCGCTGATCAGGAGGTTACAGTCCCTGTACAGACGCCCCG  
GGGGCGCGAGTCTCTCAGTATGAGCAGAGAAGCCATCAGACTCAACGAACAGTCTGTGGAGGATTCCTCAAGT  
TGCCCCGGGCGCGGTTGCGCTTGGCTGGGAGATCGTGACTCTGTGTGTGAGACCTGACTTCAGAGAGCG  
TGCCCTGCTCTCAGGGGCTGTGAATGCTGGGAGGGTCAACTGGACCTCCCTCCGCTCTGCTCTCTGTGGAA  
ACAGACCTGTGGTGCGCGGCTCTGGGAGCCTTTGGAGCAGCTGGCGTGTCTCGATTCAAGTAGGAGCCTC  
TACGACCCAGGACCAACACAGCGCTGGGCCCGAGGGTCTGGCCAAATATGGGGCGGCTCGCTAGTGTGGTGA  
CAGTGCTCTCTTATGAATACTGAGCCCTTTGTTTAAAAAACATTTCAAATGTGAACATAGAAATGAGAGGGAAG  
ATAGATGGCATGACGACAACAACGCGTCTCAGTTCTATGGCTCCGAGGGTCTGGGATGATCTCAAGTGG  
TTGTCTGAGACAGGATTTGGAACCTCTCAACACTGGCTCTCTTCACTTCCAATCTTCCGCTGCACCCGCTG  
CTGTGCTCACTGTCAGATTGAGCAGCACTTTGGGCTGGGCGGTTCTGCTTTCGCACTGAGCAGAGATGTAGTT  
TTGTGCTGCTGCTTCCCAACACTCAGGACAGAGGCTAGGTTGGCACTCGGCGCTCAGCAGGCTCTGGGCT  
GGACCCCACTCTGTGACCTTTCCAGCTGTATCAGGCTGTGGGACAACAGAGGACAGCGCAGCTCAGGAGA  
TTTCTGTGAGGATGTAGCCTTTCTCTCAGAAATCAGGGAAGAGCTGCGCTGCCCTCTCTCGTTGTTGGTGA  
GAACCCGCTGTGGCCCTTCCACCATATCAACCTGCTCATCTTTGAACTCAAAACAGGAGAACTCAACTGCA  
CTGGTCTCTCCCGAGTCCCGATTTCACCTCATCGCTCACTCTTCTCACTTCAAGGATATCAACTGAGCTGCC  
AGCAACGGGCGCTGAATTTATGTGTTTATTATACATTTTATAAGATGCACCTTTATGTCAATTTTATAAA  
GCTCGAAGATTTACTGTTTAAAAAAA

**FIGURE 142**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962

><subunit 1 of 1, 837 aa, 1 stop

><MW: 92750, pI: 7.04, NX(S/T): 6

MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLQPPPTWALSPRISLPLGSEERPFPLRF  
 EAEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKQCSFKG  
 KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVLEDDGKGRCP  
 FDPNFKSTALVVDGELYTGTVSSFQGNDDPAISRQSRLRPTKTESSLNWLQDPAFVASAYIPE  
 SLGSLQGDDDKIYFFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC  
 SRPDDGFPPFNVLDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSACVFTMKDVQRFVSG  
 LYKEVNRETQQWYTVTHPVPTPRPGACITNSARERKINSSQLPDRVLNFKDHFLLMDGQVR  
 SRMLLLQPQARYQRVAVHRVPLHHTYDVLFLGTGDGRHLKAVSVGPRVHIIEELQIFSSGQ  
 PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSSGSSCKHVSQYQ  
 QLATRPWIQDIEGASAKDLCSASSVSPSFVPTGEKPCQVQFQPNVTNTLACPLLSNLATR  
 LWLRNGAPVNASASCHVLPTGDLVLTGTLGQQLGFEQCSWLEEGFQQLVASYCPEVVEDGVADQ  
 TDEGGSVPVPIISTSRVSAPAGGKASWGADRSYWKFLVMCTLFVLAVLLPVFLFLYRHRNSM  
 KVFLKQGECAVHFKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKR  
 PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

**Transmembrane domains:**

amino acids 23-46 (type II), 718-738

# FIGURE 143A

CTAAGCCGAGGATGTGCAGTTCGCGCGCGCGCGCGGCTACGAAGAGACGGGGACAGGCGCGGTGCGAACCGA  
GCCCGCCAGCCGAGAGACGCGGGCAGGCGGGAGCCGGAGCTCGTTCGCCCGCCGCTCGTCGCGCGTGC  
TGCCCGCCCGCGCTCCCGCGCGCGCGGGAGGGCCGCCGACCTCGCGCCGAGCGCGCGCTAGCGCGCGC  
CGGGCATGGTCCCTCTTTAAAGGCGCAGGCGCGCGCGCGGGCGGGTGTGCGGAACAAAGAGCGCGCGCGGG  
CCTGCGGCGCGTCTGGGGCGCGCATGCGCGCGCGCGGGCCGCGCGCGCGCGCGCGCTCCCGCGCGCGCGCTCG  
CGCGCTTAGGGCGGGCTGGCCCTCGTGGCGGGGCGACGCGGCTGAGGGCGCGCGGAGCGTCTGGCGCGCGCGG  
CGCGCGCGCGCGCGCGCGCGGGAGCGCGCGGGC**ATG**CGCGCGCGCGCGCGCGCGCGCGCGCTGGCTTCAGGCTGC  
TGCTCGCGGCTCGTCTGGGCTTCGTGCTGGCTCGCGGCTCGTCTGCCCGGGGCTCCGAGTGAAGCGAGCGG  
GCCCGCCGCGCGCGCGCGCGCGCGGGCTGCCGCTCGCGCGAGCGCGCGCTCCGAGCGCGCGCGCGCGCG  
GCGATCGCGCGGGGCGCAGCTCTGGCGCGCGCGCTCGGACCCAGATGGCGGCGCGCGCGCAGGAACCTTCTCT  
TCGTGGGAGTCATGACCGCCAGAAATACCTGCAGACTCGGGCCGTGGCCGCTACAGAACATGGTCCAGAGCAA  
TTCTCGGGAAAGTTCAGTCTTCTCAAGTGAGGGTCTGCACATCTGTACCAATTCAGTAGTGCCACTACGGG  
GTGTGGAGACTCTACCCGCGCCAGAGAAGTCTTCATGATGCTCAAGTACATGCACGACCACTACTTGGACA  
AGTATGAATGGTTTATGAGAGCAGATGATGACGTGATCATCAAGAGAGACCGTCTGGAGAACTCTCTGAGGAGT  
TGAACAGCAGCGAGCGCTCTTCTTGGGACAGAGGCTTGGGACACCGGAAGAAATGGGAAACTGGCCCTGG  
ACCTTGGTGAAGATCTTCGATGGGGGGGCTGGCGTATCATGAGCGGGAGGTGCTTCGGAGAAATGGTGGCGC  
AGCTTGGCAAGTGTCTCCGGGAGATGTACACACCAATGAGGACTGAGGAGCTGGAGTGGGAGGTGTGTCGGAGGT  
CAGGGGTGCGAGTGTCTGGTCTTATGAGATCGCGGAGCTTTTATGAGAATTCAGCGACGACAAAGGGGT  
ACATTAGAGATCTCCATGAGAGTAAATTCACCAAGCTATACATTACACCAACAAAGACCACTTCCAGCT  
ACAGGCTCCACAGCTACATCTGACGCGCAAGATATCCGAGCTCCGCGCATCGCAACATACAGCTCGACCGGAAA  
TTGTCTGATGAGCAAACTGACGACCAACAGAAATTCATAAAGAGGACTCCAGCTGGGAATCTCCCTCTTCA  
TGAGTGTTCAGCGCCCGCAGAGAGATCTTGGAAATGGAGTTCCTGACTGGAAATATCTGTATCTCGCAG  
TTAGCGCGCAGCCCTCTCAAGAGAAATGGACTTCGCCCGACAGGAGCGCTTGAGCAGACTTGTCTGAGCTCA  
TGGAGATGATCAATGCCAACGCCAAGACAGAGCGCGCATCATTGACTTCAAGAGATCCAGTACGCGTACCGCC  
GGGTGAACCCCATGTATGGGCTGAGTACATCTCGGACCTGCTGCTCTGTACAAAGACCAAGGAGGAAAGAA  
TGACGCTCCCTGTGAGGAGCGACCGTATTACAGCAGACTTTCAGCAAAATCCAGTTTGTGGAGCATGAGGAG  
TGGATGCACAAGAGTTGGCCAGAGGAATCAATCAGGAATCTGGATCTTGTCTCTTCTCCAACTCCCTGAAGA  
AGCTCGTCCCTTTTCAGCTCCCTGGGTCGAAGAGTGAGCACAAAGACCCAAAGATATAAGACATACATCTGA  
TTCTCTTGTCTGGGCTTTTCGACATGTTGTGAGATTTATGGGAAACTTTGAGAAACAGGTGTCTTATCCCAATC  
AGAAGCTCAAGCTCGTGGTCTGCTTTTCAATCTGACTCCAACCTTGACAAGGCGCAACAAAGTTGAATGATGA  
GAGATTACCGCATTAAGTACCTTAAAGCCGACATGCAGATTTCGCTGTGTCTGGAGAGTTTTCAGAGCCCTCG  
CCCTGGAAGTAGGATCTCCAGTTTAAACATGAATCTTTGCTCTCTCTGCGAGCTGCAGCTCGTGTTTTACTA  
CAGAAATCTCTCAGCGATGTGAGCAAAATACAGTTCTGGGCGCAACAAATATATTTTCCAAATCATCTTCAGCCAGT  
ATGACCCAAAGATTGTTTATAGTGGGAAAGTTCCAGTGACAAACCATTTTGGCTTTTACTCAGAAAACTGGCTCT  
GGAGAAATATGGGTGGGATCAGGTGATTTTAAAGGGAGATCTGTCCGAGTGGGTGGCTTTGATGTTTCCA  
TCCAAGGCTGGGGCTGGAGATGTGGACCTTTTCAACAAGGTTGTCCAGGCGAGTTTGAAGACGTTTAGGAGCC  
AGGAAGTAGGAGTAGTCCAGCTCCACCATCTGTCTTTTGTGATCCAATCTTGACCCCAACAGTAGTACAAATGT  
GCTTGGGTTCCAAAGCATCGACCTATGGGTCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAATGATCCAA  
GTTACAGTAAAGCAGCAATAATAATGGCTCAGTGAGGACAGCC**TA**ATGTCCAGCTTTGCTGGAAAAAGCGTTT  
TAATTATCTAATTTATTTTCAAAAATTTTGTATAGTCAGTTTCTGAAGTCGGATATACAAGGATATATTTTAC  
AAGTGGTTTCTTACATAGGACTCTTAAAGATTGAGCTTCTGAACAGAGAGGTGATCAGTGTTCGCTTTGAA  
CACATCTCTTCTGGAACATTTATGTAGCAGACCTGCTTAATCTTGACTTGAATGTACCTGATGAACAAACCTT  
TTTTAAAAATGTTTCTTCTTGAGACCTTTTGTCCAGTCTTATGGCAGAAACGTTGAACATCTCTGCAAGAT  
TATTGTGACAAACAGCATGTAACCTCGTGAATAAGTTCTGTTGTGATTGTTAACTTCCACAGATTCTACCTTTGT  
GTTTGTGTTTTTTTTTAACTATTGTTTAAAGCCATTTCATGTTCCAGTTGTAAGATAAGGAAATGTGATATA  
GCTGTTTTCATCATGTCTCTCAGGAGAGCTTCCAGAGTTGATCATTTCTCTCATGGTACTCTGCTCAGCATGGC  
CAGTAGGTTTTTTGTTGTTGTTGTTGTTCTTTTTTGAAGCGGAGTCTCATCTGTATCCAGCGCTGGAATG  
CAGTGGCGAATCTTGGCTCACTTTTAACTCCACTTCCCTGGTTCAAGCAATCCCTGCTTGGCTCGCTCGG  
AGCTGGGATTCAGGCGACACACCCAGCCAGTGTATTTTGTATTTTGTAGTAAAGCGGGGTTTACCAT  
CGAAGCCAGCTGGCCACGTAGGTTTTTAAAGCAGGGGCGTGAAGAGGCAGTGAGGATGTGGCTGTCTCG  
TGGTAGTCTATTTCGCGCTAAATAGACCTGGCATTAATTTCAAGAAGGATTGGCATTTCTCTTCTGACCTT  
CTCTTTTAAAGGTAAATATTAATGTTTGAATGACAAAGATGAATATACAAATAATCTGATACAGACT  
GAAACATACACACATACACCTTAATCAAACGTTGGGAAAAATGTATGGTTTGTGCTCTTCATCTGCTGCT  
TTGTATGCGGTGGAGATGGTTTCTATTCTTTCACTAGCTGTTTGTGTTTGTATCTGAAATACCTTTAA  
TTTATTTAATATCTGTTGTTTCAGAGCTCTGCCATTCTTGAGTACCTGTTAGTTAGTATTTATTTATGTGATCGG  
GAGTGTGTTTGTCTGTTTATTTTCAGTAAACGATCTCCAAGATTTCCTTTTGGAAAGCGCTTTTCCCTCTC



**FIGURE 143B**

TTAATTTTATATTCCTTACTGTTTACTAAATATTAAGTCTTCTTGACAATTTTGGTGCTCATGTTTGGG  
GACAAAGTGAAATGAATCTGTCATTATACCAGAAAGTTAAATCTCAGATCAAATGTGCCTTAATAAATTTGTT  
TTCATTTAGATTTCAAACAGTGATAGACTTGCCATTTTAAATACAGTCATTGGAGGGCTGCGTATTTGTAAATAG  
CCTGATGCTCATTTGGAAAAATAACCAAGTGAACATATTTTCTATTTGTACTTTTCGAACCATTTTGTCTCATT  
ATTCTGTTTTAGCTGAAGAATTGTATTACATTTGGAGAGTAAAAAAGTTAAACACGAAAAA

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**FIGURE 144**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836  
><subunit 1 of 1, 802 aa, 1 stop  
><MW: 91812, pI: 9.52, NX(S/T): 3  
MAARGRRAWSVLLGLVLGFVLASRLVLPRASELKRAGPRRRASPEGCRSGQAAASQAGGAR  
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAAYRTWSKTI PGKVQFSSSEG  
SDTSVPIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEWFMRADDDVYIKGDRLENFLR  
SLNSSEPLFLGQTGLGTTEEMGKLALPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT  
THEDVEVGRCVRRFAGVQCWWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP  
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDLQLGIPPSFMRFPQPRQEE  
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY  
GYRRVNPMYGAEYILDLLLYKKHKGKKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR  
INQESGSLSFLSNLSLKKLVFPQLPGSKSEHKPEPKDKKINILIPLSGRFDMFVRFMGNFECTC  
LIPNQNVKLVVLLFNSDSNPDKAKQVELMRDYRIKYPKADMQILFVSGEFSRALALEVGSSQ  
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT  
QKTGFWRNYGFGITCIYKGDIVRVGGFDVSIQGWGLEDDVLEFNKVQAGLKTFRSQEVGVVH  
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA

**Signal peptide:**

amino acids 1-23

**FIGURE 145**

GGACAACCGTTGCTGGGTGTCCAGGGCCTGAGGCAGGACGGTACTCCGCTGACACCTTCCC  
 TTTCGGCCTTGAGGTTCCAGCCTGGTGGCCCCAGGACGTTCCGGTCGCATGGCAGAGTGCT  
 ACGGACGACGCCCT**ATGA**AGCCCTTAGTCCTTCTAGTTGCGCTTTTGCTATGGCCTTCGCTCG  
 TGCCGGCTTATCCGAGCATAACTGTGACACCTGATGAAGAGCAAACTTGAATCATTATATA  
 CAAGTTTTAGAGAACCTAGTAGCAAGTGTTCCCTCTGGGGAGCCAGGTCGTGAGAAAAATC  
 TAACTCTCCAAAACATGTTTATTCTATAGCATCAAAGGGATCAAAATTTAAGGAGCTAGTTA  
 CACATGGAGACGCTTCAACTGAGAATGATGTTTTAACCAATCCTATCAGTGAAGAAACTACA  
 ACTTTCCCTACAGGAGGCTTCACACCGGAAATAGGAAAGAAAAACACACGGAAAGTACCCC  
 ATTCTGGTCGATCAAACCAACAATGTTTCCATTGTTTTGCATGCAGAGGAACCTTATATTG  
 AAAATGAAGAGCCAGAGCCAGAGCCGGAGCCAGCTGCAAAACAACTGAGGCACCAAGAATG  
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATAAAGTCACCTGTAC  
 CACTTTAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCTCAGCTCT  
 CAGGTGAACTGCGATAGAAAAACCCGAAGAGTTTGAAAGCACCCAGAGAGTTGGAATAAT  
 GATGACATTTTGAAAAAATTTTAGATATTAATTCACAAGTGCAACAGGCACCTCTTAGTGA  
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAACGAAGCC  
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA  
 GTAGGACGAACAAGTAATAAAATTTGATGACATCGAACTGTTATTAAACATGCTGTGTAATTC  
 TAGATCTAACTCTATGAATATTTAGATATTAATGTGTTCCACCAGAGATGAGAGAAAAAG  
 CTGCTACAGTATTCAATACATTAAAAAATATGTGTAGATCAAGGAGAGTCACAGCCTTATTA  
 AAAGTTTAT**TAA**ACAATAATATAAAAAATTTTAAACCTACTTGATATTCATAACAAGCTGA  
 TTTAAGCAAAGTGCATTTTTTACAGGAGAAATAATCATATTCGTAATTTCAAAGTTGTAT  
 AAAAAATATTTCTATTGTAGTCAAATGTGCCAACATCTTTATGTGTATGTGTTATGAACA  
 ATTTTCATATGCACTAAAAACCTAATTTAAAAATAAAATTTTGTTTCAGGAAAAA

**FIGURE 146**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVLLVALLLWFPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPVSGEPGREKKSNSPK
HVYSIASKGSKFKELVTHGDASTENDVLTNPISSETTTFPTGGFTPEIGKKKHTESTPFWSI
KPNNVSIVLHAEOPYIENEEPEPEPEPAKQTEAPRMLPVVTESSSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSALAAAAEHKLKTMYSQLLPVGRTSNKIDDIE TVINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

**Signal peptide:**  
amino acids 1-19

**FIGURE 147**

CGGCTCGAGCGGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG  
 ACCTCCAAATCATCCATCCACCCCTGCTGTCATCTGTTTTCATAGTGTGAGATCAACCACAC  
 GGAATATCC**ATG**GGCTTTTGTGCTCATTTTGGTTCTCAGTTTCTACGAGCTGGTGTGAGGACA  
 GTGGCAAGTCACTGGACCGGCAAGTTTGTCCAGGCCTTGGTGGGGGAGGACGCCGTGTTCT  
 CCTGCTCCCTCTTTTCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCCTCAGGAATCAG  
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAGACTGGGAATCTAAGCAGATGCCACA  
 GTATCGAGGGAGAAGTGAAGTGTGTAAGGACTCCATTGCAGGGGGGCGTGTCTCTCTAAGGC  
 TAAAAAATCACTCCCTCGGACATCGGCCTGTATGGGTGCTGGTTCAGTTCAGATCCAGATTTAC  
 GATGAGGAGGCCACTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTTCCTCTCATTTCCAT  
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCTCAGGCTGGTTCCTCCCGAGC  
 CCACAGCCAAGTGGAAAGTCCACAAGGACAGGATTGTCTTCAGACTCCAGAGCAAAATGCA  
 GATGGGTACAGCCTGTATGATGTGGAGATCTCCATTATAGTCCAGGAAAAATGCTGGGAGCAT  
 ATTGTGTTCCATCCACCTTGTGAGCAGAGTCACTGAGGTGGAATCCAAGGTATTGATAGGAG  
 AGACGTTTTTCCAGCCCTCACCTTGGCGCCTGGCTTCTATTTTACTCGGGTACTCTGTGGT  
 GCCCTGTGTGGTGTGTGATGGGGATGATAATTGTTTTCTTCAAATCCAAAGGAAAAATCCA  
 GGCGAACTGGACTGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCCGGAAACAGC  
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCCGAAGCTCTGCGTTTTCTGATCTGAAA  
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA  
 GAGTGTGGTGGCTTCTCAGGGTTTCCAAGCAGGGAGACATTATGGGAGGTGGACCTGGGAC  
 AAAATGTAGGGTGGTATGTGGGAGTGTGTGGGATGACGTAGACAGGGGGAAGAACAATGTG  
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACAATTTGTATTTTCA  
 ATTCAATCCCCATTTTATCAGCCTCCCCCAGCACCCCTCTACACGAGTAGGGGTCTTCC  
 TGACTATGAGGGTGGGACCATCTCCTTCTTCAATACAAATGACCAGTCCCTTATTTATACC  
 CTGCTGACATGTCAGTTTGAAGGCTTGTGAGACCCCTATCCAGCATCGGATGTATGACGA  
 GGAAAAGGGGACTCCCATTATCATATGTCCAGTGTCTTGGGGAT**TGA**GACAGAGAAGACCCCTG  
 CTTAAAGGGCCCCACACCACAGACCCAGACACAGCCAAGGGAGAGTGCTCCCGACAGGTGGC  
 CCCAGCTTCTCTCCGGAGCCTGCGCACAGAGAGTCAAGCCCCCACTCTCCTTTAGGGAGC  
 TGAGGTCTTCTGCCCCGAGCCCTGCAGCAGCGGCAGTCACAGCTTCCAGATGAGGGGGGAT  
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAATAGACTCA  
 CATTAGGTTTGTGTTGTGAAAACTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC  
 CAGGCTCCTCATTTGTCTAGTCAAGGACAGTGATTCTGCTCCTCACAGGTGAAGATTAAAGAGA  
 CAACGAATGTGAATCATGCTGTGAGGTTTGAAGGCACAGTGTTTGCTAATGATGTGTTTTTA  
 TATTATACATTTTCCCACCTAACTCTGTTTGCTTATTTCCACATTAATTTACTTTTCTCTA  
 TACCAATACCCCATGGAATAGTTATTGAACACCTGCTTTGTGAGGCTCAAGAAATAAAGAG  
 GAGGTAGGATTTTTCAGTGAATCTATAAGCCAGCATTACCTGATACCAAAACAGGCAAG  
 AAAACAGAAGAAGAGGAAGGAAAACTACAGGTCCATATCCCTCATTAACACAGACACAAAAA  
 TTCTAAATAAAATTTTAAACAAATTAACATAACATATATTTAAAGATGATATATACTACT  
 CAGTGTGGTTTTGTCCCAAAATGCAGAGTTGGTTAAATATTTAAATTAACCCAGTGAAT  
 CAGCACATTAATAAAGTAAAAAGAAACCATAAAAA

**FIGURE 148**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866  
><subunit 1 of 1, 466 aa, 1 stop  
><MW: 52279, pI: 6.16, NX(S/T): 2  
MAFVLILVLSFYELVSGQWQVTGPGKFVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA  
VVHLYRDGEDWESKQMPQYRGRTEFVKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE  
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFPQPTAKWKGPQGQDLSSDSRANADGY  
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVLIGETFFQPSPWRLASILLGLLCGALC  
GVVMGMIIVFFKSKGKIQAELDWRKKGQAELRDARKHAVEVTLDPETAHPKLCVSDLKTVT  
HRKAPQEVPHSEKRFTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS  
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRVGVFLDYEGGTISFFNTNDQSLIYTLLT  
CQFEGLLRPYIQHAMYDEEKGTFIFICPVSWG

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 131-150, 235-259

**FIGURE 149**

CCTTCACAGGACTCTTCATTGCTGGTTGGCAATGATGTATCGGCCAGATGTGGTGAGGGCTA  
 GGAAAAGAGTTTGTGGGAACCCCTGGGTATCGGCCCTCGTCATCTTCATATCCCTGATTGTC  
 CTGGCAGTGTGCATTGGACTCACTGTTTATTATGTGAGATATAATCAAAAAGAGACCTACAA  
 TTAATAATAGCACATTGTCTTACAACTGACAACTATATGCTGAGTTTGGCAGAGAGGCTT  
 CTAACAATTTTACAGAAATGAGCCAGAGACTTGAATCAATGGTGAAAAATGCATTTTATAAA  
 TCTCCATTAAAGGAAGAAATTTGTCAAGTCTCAGGTTATCAAGTTCAGTCAACAGAAGCATGG  
 AGTGTGGCTCATATGCTGTTGATTGTAGATTTCATCTACTGAGGATCCTGAAACTGTAG  
 ATAAAATTGTTCAACTTGTGTTTACATGAAAAGCTGCAAGATGCTGTAGACCCCTTAAAGTA  
 GATCCTCACTCAGTTAAAATTAATAAATCAACAAGACAGAAACAGACAGCTATCTAAACCA  
 TTGCTGCGGAACACGAAGAAGTAAACTCTAGGTCAGAGTCTCAGGATCGTTGGTGGGACAG  
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGGATGGGAGTCATCGCTGT  
 GGAGCAACCTTAATTAATGCCACATGGCTTGTGAGTGTCTCACTGTTTTACAACATATAA  
 GAACCTGCCAGATGGACTGCTTCCCTTTGGAGTAACAATAAACCTTCGAAAAATGAACGGG  
 GTCTCCGGAGAATAATTGTCCATGAAAAATACAACACCCATCACATGACTATGATATTTCT  
 CTTGCAGAGCTTTCTAGCCCTGTTCCCTACACAATGCAGTACATAGAGTTTGTCTCCCTGA  
 TGCATCCTATGAGTTTCAACCAGGTGATGTGATGTTTGTGACAGGATTGGAGCACTGAAAA  
 ATGATGGTTACAGTCAAAATCATCTTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC  
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCTT  
 AGAAGGAAAAACAGATGCATGCCAGGTGACTCTGGAGGACCACTGGTTAGTTCAGATGCTA  
 GAGATATCTGGTACCTTGTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCACAAG  
 CCTGGTGTATATACTAGAGTTACGGCCTTGCGGGACTGGATTACTTCAAAAACCTGGTATCTA  
AGAGACAAAAGCCTCATGGAACAGATAACATTTTTTTTTGTTTTTGGGTGTGGAGGCCATT  
 TTTAGAGATACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTCAATAAAC  
 TGTTTGCTTGATGCATGTATTTCTTCCAGCTCTGTTCCGACGTAAGCATCCTGCTTCTG  
 CCAGATCAACTCTGTCATCTGTGAGCAATAGTTGAAACTTTATGTACATAGAGAAATAGATA  
 ATACAATATTACATTACAGCCTGTATTCAATTTGTTCTCTAGAAGTTTTGTGAGAATTTGAC  
 TTGTTGACATAAATTTGTAATGCATATATACAATTTGAAGCACTCCTTTCTTCAGTTCCTC  
 AGCTCCTCTCATTTCAGCAAATATCCATTTTCAAGGTGCAGAACAGGAGTGAAAGAAAATA  
 TAAGAAGAAAAAATCCCTACATTTTATTGGCACAGAAAAAGTATTAGGTGTTTTTCTTAGT  
 GGAATATTAGAAATGATCATATTCATTATGAAAGGTCAAGCAAAGACAGCAGAATACCAATC  
 ACTTCATCATTTAGGAAGTATGGGAAGTAAAGTTAAGGAAGTCCAGAAAGAAGCCAAGATATA  
 TCCTTATTTTCATTTCCAACAACACTACTATGATAAATGTGAAGAAGATTCTGTTTTTTTGTG  
 ACCTATAATAATTATACAACCTCATGCAATGTACTTGTCTTAAGCAAATTAAGCAAATAT  
 TTATTTAACATTGTTACTGAGGATGTCAACATATAACAATAAAATATAAATCACCCA

**FIGURE 150**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTYNYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAFYKSPLREEFVKSQVIKFSQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPQWASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPSHDYDISLAELSSPVPTYNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSONHLRQAQVTLIDATTCNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTGI

```

**Transmembrane domain:**

amino acids 21-40 (type II)



**FIGURE 151**

GTCGAAGGTTATAAAAGCTTCCAGCCAAACGGCATTGAAGTTGAAGATACAACCTGACAGCA  
 CAGCCTGAGATCTTGGGGATCCCTCAGCCTAACACCCACAGACGTCAGCTGGTGGATTCCCG  
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTTCTGTGGCTCCTGGC  
 CGTGACCTTCTTGGTTCCAGAGCTCAGCCCTTGGCCCCCTCAAGACTTTGAAGAAGAGGAGG  
 CAGATGAGACTGAGACGGCGTGCCCGCCTTTGCCGGCTGTCCCTGCGACTACGACCACTGC  
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCGGCCTGCCTGTGCC  
 AGGACTCTCCAGCCCCGCCAGCCGCCGACCCGCCGCGCATGGGAGAAGTGCGCATTGCGG  
 CCGAAGAGGGCCGCGCAGTGGTCCACTGGTGTGCCCCCTTCTCCCGGTCTTCCACTACTGG  
 CTGCTGCTTTGGGACGGCAGCGAGGCTGCGCAGAAGGGGCCCCCGCTGAACGCTACGGTCCG  
 CAGAGCCGAAGTGAAGGGGCTGAAGCCAGGGGGCATTATGTCTGTTTGGTAGTGGCCGCTA  
 ACGAGGCCGGGGCAAGCCGCGTGCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGGCCGACATC  
 CCTGCCCTTCGGGCCTTGACGCGCCTTGCGGTGCCGCCAACCCCGCACTCTGGTCCACGC  
 GGCCGTCGGGTGGGCACGGCCCTGGCCCTGCTAAGCTGTGCCGCCCTGGTGTGGCACTTCT  
 GCCTGCGCATCGCTGGGGCTGCCCGCGCCGAGCCGCCGCCGAGCCGCAGGGGCGCT**TGA**  
 AAGGGGCTGGGGCATCTCGGGCACAGACAGCCCACTGGGGCGCTCAGCCTGGCCCCCG  
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGGAGCCAGCCCCAG  
 GCTCCAGGGCCACGGCGAGTCATGGTTCTCAGGACTGAGCGCTTGTTTAGGTCCGGTACTT  
 GCGCCTTTGTTCTTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTTTTTA  
 AGCGGCCAGATAATAATAATGTAACTTTGCGGTTAAAAAAAAAAAAAAAAAAAA

**FIGURE 152**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQFLAPQDFEEEEADETETAWPPLPAVPCDYDHCRLQVPCKE
LQRVGPAACLCPLGSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLWDGSEA
AQKGPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVQPAGGEGLEGADIPAFGPCSRL
AVPPNPRTLVAAGVGTALALLScaalVWHFCLDRDRWGCPRRRAARAAGAL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 194-220

**N-glycosylation site.**

amino acids 132-135

**FIGURE 153**

AGAGAAAGAACGCTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC  
 CTGCCCGCATGAGCCCCCGCGTGCCTCCCCGACTATCCCCAGGCGGGCGTGGGGCACC  
 CCCAGCGCGACGATCGCTGCCGTTTGGCCCTTGGGAGTAGGATGTGGTGAAGGATGGGCG  
 TTCTCCCTTACGGGGCTCACAAATGGCCAGAGAAGATTCCTGTGAAGTGTCTGCGCTGCCTGCT  
 CTACGCCCTCAATCTGCTCTTTTGGTTAATGTCCATCAGTGTGTTGGCAGTTTCTGCTTGA  
 TGAGGGACTACCTAAATAATGTTCTCAGTTTAACTGCAGAAACGAGGGTAGAGGAAGCAGTC  
 ATTTTGACTTACTTTCTGTGGTTTCATCCGGTCATGATTGCTGTTTCTGCTGTTTCTTATCAT  
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAGAAATCTGTTGCTTCTTGCATGGTACT  
 TTGGAAGTTTGCTTGTCAATTTCTGTGTAGAAGTGGCTTGTGGCGTTTGGACATATGAACAG  
 GAACCTATGGTCCAGTACAATGGTCAGATATGGTCACCTTTGAAAGCCAGGATGACAAATTA  
 TGGATTACCTAGATATCGGTGGCTTACTCATGCTTGGAAATTTTTTTCAGAGAGAGTTTAAAT  
 GCTGTGGAGTAGTATATTTTCACTGACTGGTTGGAATGACAGAGATGGACTGGCCCCCAGAT  
 TCCTGCTGTGTTAGAGAATTTCCAGGATGTTCCAAACAGGGCCACCAGGAAGATCTCAGTGA  
 CCTTTATCAAGAGGGTTGTGGGAAGAAATGTATTCTTTTTCAGAGGAACCAACCACTGC  
 AGGTGCTGAGGTTTCTGGGAATCTCCATTGGGGTGACACAAATCTGGCCATGATTCTCACC  
 ATTACTCTGCTCTGGGCTCTGTATTATGATAGAAGGAGCCTGGGACAGACCAATGATGTC  
 CTTGAAGAATGACAACTCTCAGCACCTGTCATGTCCCTCAGTAGAACTGTTGAAACCAAGCC  
 TGTCAAGAATCTTTGAACACACATCCATGGCAACAGCTTTAATACACACTTTGAGATGGAG  
 GAGTTATTAAGAAAGAAATGTACAGAAGAAACCAACAACTGTTTATTGGACTTGTGAAT  
 TTTGAGTACATACTATGTGTTTCAGAAATATGTAGAATAAAAAATGTTGCCATAAAATAACA  
 CCTAAGCATATACTATTCTATGCTTTAAATGAGGATGGAAAGTTTCATGTCATAAGTCAC  
 CACCTGGACAATAATTTGATGCCCTTAAATGCTGAAGACAGATGTCATACCCACTGTGTAGC  
 CTGTGTATGACTTTTACTGAACACAGTTATGTTTTCAGGACAGCATGGTTTGTATAGCATTT  
 CGCATCCATGCAACAGAGTCACATATGGTGGGACTGGAGCCATAGTAAGGTTGATTTACTTT  
 CTACCACTAGTATATAAAGTACTAATTAATGCTAACATAGGAAGTTAGAAAATACTAATA  
 ACTTTTATTACTCAGCGATCTATTCTTCTGATGCTAATAAATATATATCAGAAAACCTTC  
 AATATTGGTGACTACCTAAATGTGATTTTTGCTGGTTACTAAAAATATTCTTACCACCTAAAA  
 GAGCAAGCTAACACATTTGCTTAAAGCTGATCAGGATTTTTTGTATATAAGTCTGTGTAAA  
 TCTGTATAATTGAGTCGATTTTCAGTTCTGATAATGTTAAGAAATACCATTTATGAAAGGAAA  
 ATTTGTCTGTATAGCATCATATTATTTAGCCTTTCCTGTTAATAAAGCTTTACTATTCTGT  
 CCTGGGCTTATATTACACATATACTGTTATTAAATACTTAACCACTAATTTTGAATTA  
 CCAGTGTGATACATAGGAATCATTATTAGAATGTAGTCTGGCTTTAGGAAGTATTATATAA  
 GAAAATTTGCACATACTAGTTGATTGATTGAGAAAGGACTTGTATGCTGTTTTCTCCCAATG  
 AAGACTCTTTTTCAGACTTAAACACTTTTTTAAAGGCTTATCTTTGCCCTTCTCAACAAAGAA  
 GCAATAGTCTCCAGTCAATATAAATCTACAGAAAATAGTGTCTTTTCTCCAGAAAAAT  
 GCTTGTGAGAATCATTAACATATGTGACAAATTTAGAGATTCTTTGTTTTATTTTCACTGATTA  
 ATATACTGTGGCAAAATACACAGATTATTAATTTTTTTTACAAGAGTATAGTATATTTATTT  
 GAAATGGGAAAAGTGATTTTACTGTATTTTGTGATTTTTGTTTTATTTCTCAGAATATGGAA  
 AGAAAATTAATGTTGTCATAAATATTTTCTAGAGAGTAA

**FIGURE 154**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAVSAWMRDYLNNVLTTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLLLLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVVYFTDWLEMTENDWPPDSCCVREF
PGCSKQAHQEDLSLDLYQEGCGKKMYSFLRGTKQLQVLRFLGISIGVTQILAMILTITLLWAL
YYDRREP GTDQMMSLKNDNSQHLSCPSVELLKP SLSRIFEHTSMANSFNTHFEMEEL
```

**Signal peptide:**

amino acids 1-33

**Transmembrane domains:**

amino acids 12-35, 57-86, 94-114, 226-248

**FIGURE 155**

GAGAGAGGCAGCAGCTTGCTCAGCGGACAAGGATGCTGGGCGTGAGGGACCAAGGCCTGCCC  
 TGCACCTCGGGCCTCCTCCAGCCAGTGTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA  
 CCTGTGTGGGGAGGCCCTCCTGCTGCCTTGGGGTGACAATCTCAGCTCCAGGCTACAGGGAG  
 ACCGGGAGGATCAGAGAGCCAGC**ATG**TTACAGGATCCTGACAGTGATCAACCTCTGAACAGC  
 CTCGATGTCAAACCCCTGCGCAAACCCCGTATCCCCATGGAGACCTTCAGAAAGGTGGGGAT  
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGTCTCATCAAGG  
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCCGAGGAAGCAG  
 CTGTGTGACGGAGAGCTGGACTGTCCCTTGGGGGAGGACGAGGAGCACTGTGTCAAGAGCTT  
 CCCCAGAGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG  
 ACTCGGCCACAGGGAAGCTGGTTCTCTGCCTGTTTCGACAACCTTCACAGAAGCTCTCGCTGAG  
 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCCAGACCAGGATCTGGA  
 TGTGTGTGAAATCACAGAAAACAGCCAGGAGCTTCGCATGCGGAACCTCAAGTGGGCCCTGTCT  
 TCTCAGGCTCCCTGGTCTCCCTGCAGTGTCTTGCTGTGGGAAGAGCCTGAAGACCCCCCGT  
 GTGGTGGGTGGGAGGAGCCCTCTGTGGATTCTTGGCCTTGGCAGGTGAGCATCCAGTACGA  
 CAAACAGCACGTCTGTGGAGGGAGCATCCTGGACCCCCACTGGGTCTCACGGCAGCCCCACT  
 GCTTCAGGAAACATACCGATGTGTTCAACTGGAAGGTGCGGGCAGGCTCAGACAACTGGGC  
 AGCTTCCCATCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCCATGTACCCCAA  
 AGACAATGACATCGCCCTCATGAAGCTGCAGTTCCTACTACTTTCTCAGGCACAGTCAGGC  
 CCATCTGTCTGCCCTTCTTTGATGAGGAGCTCACTCCAGCCACCCCACTCTGGATCATTGGA  
 TGGGGCTTTACGAAGCAGAATGGAGGGAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA  
 GGTCATTGACAGCACACGGTGCAATGCAGACGATGCGTACCAGGGGGAAGTCACCGAGAAGA  
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTGACAGTGGTGGGCC  
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGGCATCGTTAGCTGGGGCTATGGCTGCGG  
 GGGCCCGAGCACCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG  
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCCCTTTCAGTGTGGGAGCCGCTTCCTTCTCTG  
 CCCTGCCACCTGGGGATCCCCCAAAGTCAGACACAGAGCAAGAGTCCCTTGGGTACACCC  
 CTCTGCCCCAGCCCTCAGCATTTCTTGGAGCAGCAAAGGCCCTCAATTCTGTGAAGAGACCC  
 TCGACGCCAGGAGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTTGGTGTCTCC  
 AGCATCCAGGGAGAGACACAGCCCACTGAACAAGGTCTCAGGGGTATTGCTAAGCCAAGAA  
 GGAACCTTCCCACACTACTGTAATGGAAGCAGGCTGTCTTGTAAGGCCAGATCACTGTGGG  
 CTGGAGAGGAGAAGGAAGGGTCTGCGCCAGCCCTGTCCGTCTTACCCATCCCCAAGCCTA  
 CTAGAGCAAGAAACAGTTGTAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT  
 ACCTACTGTTGTCTATTGTTATTACAGCTATGGCCACTATTATTAAAGAGCTGTGTAACATCT  
 CTGGCAAAAAAAAAA

**FIGURE 156**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885  
><subunit 1 of 1, 432 aa, 1 stop  
><MW: 47644, pI: 5.18, NX(S/T): 2  
MLQDPDSQQPLNSLDVKPLRKPRIPMETFRKVGIPIIIALSLASIIIVVLIKVILDKYYF  
LCGQPLHFI PRKQLCDGELDCPLGEDEEHCVKSFPEGPAAVRLSKDRSTLQVLD SATGNWF  
SACFDNFTEALAE TACRQMGYSRAVEIGPDQDL DVVEITENSQELMRNSSGPCLSGSLVSL  
HCLACGKSLKTPRVVGGEEASVDSWFPQVSIQYDKQHVC GGSILDPHWVLTAAHCFRKHTDV  
FNWKVRAGSDKLG SFPSLAVAKIIII EFNPMYPKDNDIALMKLQFPLTFSGTVRPICLPFFD  
EELTPATPLWIIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMM CAGIPE  
GGVDTCCQGD SGGLPMYQSDQWHVVGIVSWGYGCGGPSTPGVYTKVSAYLNWIYNVWK AEL

**Transmembrane domain:**

amino acids 32-53 (typeII)

**FIGURE 157**

GGGCTGAGGCACTGAGAGACCGGAAAGCCTGGCATTCACAGAGGAGGGAACGCAGCGGCATCCCCAGGCTCCAG  
 AGCTCCCTGGTGACAGCTGTGGCTGAGC**ATG**GCCCTCCCAGCCCTGGGCGCTGGACCCCTGGAGGCCTCTGGGGCC  
 TTTTCCTCTTCCAACCTGCTTCAGCTGTCTGTCGCGACGACGACCGCGGGGGAGGCGGGCAGGGGCCCATGCCCA  
 GGGTCAGATACTATGCAAGGGGATGAACGTAGGCACTTAGCTTCTTCCACGAGAAGGGCCTCCAGGATTTTGACA  
 CTCTGCTCCTGAGTGGTGATGGAATACTCTCTACGTGGGGCTCGAGAAGGCTCTTGGCCTGGGATATCCAGG  
 ATCCAGGGGTCCCGAGGCTAAAGAACATGATACCGTGGCCAGCCAGTGACAGAAAAAGATGAATGTGCCTTTA  
 AGAAGAGAGCAATGAGACACAGTGTTCACATTCATCCGTGCTCTGGTTTCTTACAATGTACCCCATCTCTACA  
 CCTGCGGCACCTTCGCCTTCAGCCCTGCTTGTACCTTCATTGAATTCACAGATTCCTACCTGTGTGCCCATCTCGG  
 AGGACAAAGTCTATGGAGGGAAAGGCCAAAGCCCTTTGACCCCGCTCACAGCATACGGCTGTCTTGGTGGATG  
 GGTGTCTTATTCTGTACTATGAACAACCTCCTGGGCAGTGAGCCCATCTGATGCGCACACTGGGATCCAGC  
 CTGTCTCAAGACCGACAACCTCCTCGCTGGCTGCATCATGACGCCCTCTTTGTGGCAGCCATCCCTTCGACCC  
 AGGTCTGTACTTCTTCTCGAGGAGACGCCAGCGAGTTTGACITCTTTGAGAGGCTCCACACATCGCGGTGG  
 CTAGAGTCTGCAAGAATGACGTGGCGGGCGAAAGCTGCTGCAGAAGAATGGACCACTTCTTGAAGGCCACG  
 TGCTCTGCAACCCAGCGGGGACGCTGCCCTTCAACGTATCCGCGCACCGCGCTCTGCTCCCGCGCATTCCCA  
 CAGCTCCCCACATCTACGAGCTTTCACCTCCAGTGGCAGGTTGGCGGGACCAGGAGCTCTGCGGTTTGTGCCT  
 TCTCTCTTTGGACATTGAACGTGTCTTTAAGGGGAAATACAAGAGTTGAACAAGAACTTCACGCTGGACTA  
 CTTATAGGGGCCCTGAGACCAACCCCGGCCAGGCACTGTCTCAGTGGGCCCCCTCTCTGATAAGGCCCTGACCT  
 TCATGAAGGACCAATTCCTGATGGATGAGCAAGTGGTGGGAGCGCCCTGCTGGTGAATCTGGCGTGGAGTATA  
 CACGGCTTGCACTGGAGACAGCCAGGGCTTGATGGGCACAGCCATCTTGTATGTACCTGGGAACCCACAG  
 GGTGCTCCCAAGGCTGTGGTAAGTGGGACAGCAGTGCTCATCTGTTGGAAGAGATTGAGCTGTTCCTTGACC  
 CTGAACCTGTTGCCAACCTGCAAGCTGCGCCCAACCCAGGGTGCAGTGTGTTGAGGCTTCTCAGGAGGTGTCTGGA  
 GGGTGCCCGGAGCCAACTGTAGTGTCTATGAGAGCTGTGTGGACTGTGTCTTGGCCCGGACCCCACTGTGCCT  
 GGGACCTGAGTCCCGAACCTGTGGCTCCTGTCTGCCCAACCTGAACCTCTGGAAGCAGGACATGGAGCGGG  
 GGAACCCAGAGTGGGCATGTGCCAGTGGCCCATGAGCAGGAGCCTTCGCGCTCAGAGCGCCGCCAAATCATT  
 AAGAAGTCTCTGGCTGTCCCAACTCCATCTTGAGCTCCCTTGCCCCACCTGTGACGCTTGGCCTCTTATTATT  
 GGAGTGTGGCCAGCAGCAGTCCCAAGGCTCTTCCACTGTCTACAATGGCTCCCTCTTGTGTGATGTGCAGG  
 ATGAGCTTGGGGTCTTACAGCTGTGGGCACTGAGAATGGCTTTTCATACCTCTGTGATCTCTACTGGGGTG  
 ACAGCCAGGACAGACCCCTGGCCCTGGATCTGAACTGGCAGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA  
 CCAGGTCAGTGTGGGGCGCCCTGGCTGCCAGCAGTCTTACTGGCCCCACTTTGTCTACTGTCACTGTCTCT  
 TTGCCTTAGTGCTTTCAGGAGCCCTCATCATCTCTGTGGCTCCCCATTGAGAGCACTCCGGGCTCGGGGCAAG  
 TTCAGGGCTGTGAGACCTCTGCCCTCTGGGAGAGGCCCGTTAAGCAGAGAGCAACACCTCCAGCTCTCCCAAG  
 AATGCAAGACCTCTGCCAGTGTGTGACGCTGACAACAACCTGACCTAGGCACTGAGGTAGCT**TAA**CTCTAGGCA  
 CAGCCCGGGCTGCGGTGCAGGCACCTGGCCATGCTGCTGGCGGCCCAAGCACAGCCCTGACTAGGATGACAG  
 CAGCACAAAGACCACTTTCTCCCTGAGAGGAGCTTCTGTACTCTGCATCACTGATGACACTCAGAGGGTG  
 ATGCACAGCAGTGTGCCTCCCCATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGCTAC  
 CCCCAGACTGTCTGCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCACTTGTGGCCATTCCAGGGACCTTC  
 CAGAAACACAGTGTTCAGAGAGCCCTAAAAAACCTGCCTGTCCAGGACCCCTATGGTAATGAACACCAACATC  
 TAAACATCATATGCTAACATGCCACTCTGGAATCCACTCTGAAGCTGCGCTTTGGACACCAACACTCCCT  
 TCTCCAGGGTCAATGAGGATCTGTCTCCTCTGCTTCCCTTACAGTCTGTGACCCGCTGACTCCAGGAAGTCT  
 TTTCTGAAGTCTGACCACTTTCTTCTGTCTCAGTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGGAATGG  
 CAGGGTAATCTGAGCCTTCTTCTGAGCTTCTTACCTTACCTAGTGACCCCTTACCTCTTCCCTTCTTCTTGT  
 TTTGGGATTGAAAACTGCTGTGTCAGAGACTGTTTATTTTTATTAAAAATATAAGGCTTAAAAAA

**FIGURE 158**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLFQLQLLLPTTTAGGGGQGFMPrVRYAGDERRALSFFHQKGLQ
DFDTLLLSGDNLTLYVGAREAILALDIQDPGVPrLKNMIPWPASDRKKSECAFKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDSFVAAIPSTQVVYFFFE
ETASEFDFFERLHTSRVARVCKNDVGGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSrWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLSHKAVVSGDSSAHLVEEIQLFDPDEPFVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVLARDPHCAWDPEsrTCCLLSAPNLNSWKQDMERGNPEWACASGPMSrSLRP
QSRPQIIKEVLAVPNsILELPCPHLSALASYWShGPAAVPEASrTVYNGSLLLIvQDGVGG
LYQCWATENGFSYpVISYWVDSQDQTLALDPELAGIPrEHVKVPLrTVSGGAALAAQqSYWP
HFVTVTVLfALVLsGALIILVASPLRALRARGKVqGCETLRpGEKAPLSrEQHLQsPKECrt
SASDVDADNNCLGTEVA
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domains:**

amino acids 136-156, 222-247, 474-490, 685-704



**FIGURE 159**

AGGGTCCCTTAGCCGGGCGCAGGGCGCGCAGCCAGGCTGAGATCCGCGGCTTCCGTAGAAG  
 TGAGC**ATGG**CTGGGCAGCGAGTGCTTCTTCTAGTGGGCTTCTTCTCCCTGGGGTCTTGCTC  
 TCAGAGGCTGCCAAATCTTGACAAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA  
 CCGGGTTTCTCAGATTCTTCAAGATCACGGTCATAATGTCACCATGCTTAACCACAAAAGAG  
 GTCC'TTTTATGCCAGATTTTAAAAAGGAAGAAAAATCATATCAAGTTATCAGTTGGGCTTGCA  
 CCTGAAGATCATCAAAGAGAATTTAAAAAGAGTTTGGATTCTTTCTGGAAGAACTTAGG  
 TGGCAGAGGAAAAATTGAAAACCTATTAAATGTTCTAGAACTACTTGGCGTTGCAGTGCAGTC  
 ATTTTTAAATAGAAAGGATATCATGGATTCCCTTAAGAAATGAGAACTTCGACATGGTGATA  
 GTTGAAACTTTTGACTACTGTCCTTTCCTGATTGCTGAGAAGCTTGGGAAGCCATTGTGGC  
 CATTCTTTCCACTTCATTGCGCTCTTTGGAATTTGGGCTACCAATCCCTTGTCTTATGTTCT  
 CAGTATTCGGTTCCTTGCTGACTGATCACATGGACTTCTGGGCGGAGTGAAGAATTTCTG  
 ATGTTCTTTAGTTTCTGCAGGAGGCAACAGCACATGCAGTCTACATTTGACAACACCATCAA  
 GGAACATTTACAGAAGGCTCTAGGCCAGT'TTTGCTCATCTTCTACTGAAAGCAGAGTTGT  
 GGTTCATTAACCTGACTTTGCTTTGATTTTGCTCGACCTCTGCTCCCAACACTGTTTAT  
 GTTGGAGGCTTGATGGA AAAACCTATTAAACAGTACCACAAGACTTGGAGAACTTCATTGC  
 CAAGTTTGGGACTCTGGTTTGTCTTGTGACCTTGGGCTCCATGGTGAACACCTGTGAGA  
 ATCCGGAATCTTCAAGGAGATGAACAATGCCTTTGCTCACCTACCCCAAGGGGTGATATGG  
 AAGTGTCAGTGTTCTCATTTGGCCCAAAGATGTCCACCTGGCTGCAAAATGTGAAATTTGTGA  
 CTGGCTTCCTCAGAGTGACCTCCTGGCTCACCCAAGCATCCGCTGTTTTGTCAACCACGGGC  
 GGCAGAAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGGATCCCTCTCTTT  
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAAGCCAAAAAGTTTGGTGTTCCTATTCAAGTT  
 AAAGAAGCTCAAGGCAGAGACATTGGCTCTTAAGATGAAACAAATCATGGAAGACAAGAGAT  
 ACAAGTCCGCGGCAGTGGCTGCCAGTGTCTATCTGCGCTCCCACCCGCTCAGCCCCACACAG  
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGCGCAGCACCTCAAGCCCTA  
 TGTCTTTCAGCAGCCCTGGCATGAGCAGTACCTGTTCCAGCTTTTGTGTTTCTGCTGGGGC  
 TCACTCTGGGACTCTATGGCTTTGTGGGAAGCTGCTGGGCATGGCTGTCTGGTGGCTGCGT  
 GGGGCCAGAAAGGTGAAGGAGACAT**TA**AGGCCAGGTGCAGCCTTGGCGGGGTCTGTTTTGGTGG  
 GCGATGTCAACATTTCTAGGGAGCTTCCCACTAGTTCTGGCAGCCCCATTCTCTAGTCTTCTC  
 TAGTTATCTCCTGTTTTCTTGAAGAACAGGAAAAATGGCCAAAAATCATCCTTTCCACTTGC  
 TAATTTTGTACAAATTCATCCTTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCTCT  
 CTGTGCTCTCTTTGTTTGGCATCAGCAAGGGCTATGCTGTGATTCTGTCTAGTCACTTG  
 GACCATGACCCTCAGATTTCCAGCCTTAAATCCACCTTCTCTCATCGCCTCTCCGAA  
 TCACACCCCTGACTCTTCAGCCTCCATGTCAGACCTAGTCAGCCTCTCTCACTCTGCCCC  
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGATATATCTTTCACTTTCTGTTT  
 GTTCTCCACATATTTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTTTCAAGGCT  
 CGGACACAGGCTCAGAGTCTCCACATTGGGTCCCTGTCTCTGGTGGCCACAGTGAGTCTCT  
 TCTTGGCTGAGCAGGCATGGAGACTGTAGGTTTCCAGATTTCTGAAAAATAAAGATTACA  
 GCGTTATCTCTCCCACTCACTAA

**FIGURE 160**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLLVGFLLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIMDSLKNENFDMVIVETFDYCPFLIAEKLKGPFAVILSTSFGSLEFGLPIPLSYVPV
FRSLTLDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTGSRPVLSHLLKAELEWF
INSDFAFDFAFARPLLENTVYVGGLEMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNAFAHLPQGVWKCQCQSHWPKDVHLAANVKIVDWLPQSDLLAHPSIRLFVTHGGQ
NSIMEAIIQHGVPMVGIPLEFGDQFENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDFVFLGLT
LGTWLWLCGKLLGMAVWWLRGARKVKET
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 483-504

**FIGURE 161**

GGGCTGTTGATTGTTGGGGGATTTTGAAGAGAGGAGGAATAGGAGGAAGGGGTTGAGGGGCT  
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGCTCACACACATACCATTGTT  
 CTCCATCCCCCAGGTCACGCCCTCAGTGCTGTCCCATCCAGCAGGGCTACCCCTGAAGCTCT  
 GGCTGCAGCCCTCCCGTCCAGTGGGCGAGCGGCTTCATCCCTCCCTTCTCTCCCAAAGCCCA  
 ACTGCTGTCACTGCATGCTCTGCCAAGGAGGAGGGAAGTGCAGTGACAGCAGGAGTAAGAGT  
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGGTTACGCCAGCCCTAGAGAGGGC  
 AGACTATCAGGGTGCCCGCGGTGAGAATCCAGGGAGAGGAGCGGAACAGAAGAGGGGCAGA  
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCCATGTTGGGAGCCAAGCCACACTGGC  
 TACCAGGTCCCTACACAGTCCCGGGCTGCCCTTGGTTCTGGTGCTTCTGGCCCTGGGGGCC  
 GGGTGGGCCAGGAGGGGTGAGAGCCCGTCTGCTGGAGGGGGAGTGCCTGGTGGTCTGTGA  
 GCCTGGCCGAGCTGCTGCAGGGGGCCCGGGGGAGCAGCCCTGGGAGAGGCACCCCTGGGC  
 GAGTGGCATTTGCTGCGGTCCGAAGCCACCACCATGAGCCAGCAGGGGAAACCGGCAATGGC  
 ACCAGTGGGGCCATCTACTTCGACAGGTCCTGGTGAACAGGGCGGTGGCTTTGACCGGGC  
 CTCTGGCTCCTTCGTAGCCCTGTCCGGGGTGCTACAGCTTCCGGTCCATGTGGTGAAGG  
 GTACAACCGCCAAACTGTCCAGGTGAGCCTGATGCTGAACAGTGGCCTGTCTCTCAGCC  
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACAGCTCTGTGCTACTGCCCTTGA  
 CCCTGGGGCCGAGTGCTCTGCGCCTGCGTGGGGGAATCTACTGGTGGTTGGAAATACT  
 CAAGTTTCTCTGGCTTCCCTCATCTTCCCTCTCTGAGGAGCCCAAGTCTTTCAAGCAAGAAT  
 CCAGCCCTTGACAACTTTCTTCTGCCCCTCTTTCGCCCAAGAACAGCAGAGGCAGGAGAGAG  
 ACTCCCTCTGGCTCCTATCCACCTCTTTGTCATGGGACCCCTGTGCCAAACACCCAAGTTTAA  
 GAGAAGAGTAGAGTGTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCCAAGTTACC  
 CTCCAGCCACCTGCTGCATCTGTTCTGCTGCAGCCCTAGGATCAGGGCAAGGTTTGGCA  
 AGAAGGAAGATCTGCACTACTTTGCGGCCCTCTGCTCCTCCGGTCCCCCAGCTTCCCT  
 GCTCAATGCTGATCAGGACAGGTGGCGAGGTGAGCCTGACAGGCCCCACAGGAGCCAG  
 ATGGACAAGCCTCAGCGTACCCTGCAGGCTTCTCCTGTGAGGAAAAGCCAGCATCACGGAT  
 TCAGCCAGCACCGCTCAGAAGCTGAGCCAGCACCGTATGGGCTAGGGTGGGAGGCTCAGCCAC  
 AGGCAGAAGGGTGGGAAGGGCCTGGAGTCTGTGGCTGGTGAGGAAGGAAGGAGGGTGTATTG  
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT  
 GGCTGTCTTCTATGCTGGATCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG  
 GGTGAGTGTTTGGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG  
 ACCATGGAAAACATCGATAACCATGCATCTCTTGTCTGGCCACCTCCTGAAACTGCTCCAC  
 CTTTGAAGTTTGAACCTTGTCCCTCCACACTCTGACTGCTGCCTCTCTCCAGGTCTC  
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTCTGAT  
 CTGTGCTGTCTTATCTCTCTCTTAGGCTTCCTATTACCTGGGATTCATGATTCAATTCCTT  
 CAGACCTCTCCTGCGAGTATGCTAAACCTCCCTCTCTTCTTATTAAGCTGTGCCATT  
 GGCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGTGCTAGTGAGACACTAT  
 AGAATTACTAAGGAGAAGATGCCTCTGGAGTTGGATCGGGTGTACAGGTACAAGTAGGTA  
 GTTTCAGAGGAAAATAATATCAAACGTATATACTAAATTAATAA

**FIGURE 162**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGLHSPGLPLVLVLLALGAGWAQEGSEPVLLGECELVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVKVYNRQTVQVSLMLNTWFPVISAFANDPDVTREAAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
```

**Signal peptide:**  
amino acids 1-32

**FIGURE 163**

**FIGURE 164**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184  
><subunit 1 of 1, 388 aa, 1 stop  
><MW: 43831, pI: 9.64, NX(S/T): 3  
MKTLLAAYSGVLRGERQAEADRSQQRSHGGPALSREGSGRWGTGSSILSALQDLFSVTWLNRS  
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIADVLYFTWLVDWNTPKKGGRRS  
QWVRNWAVWRYFRDYFPIQLVKTHNLLTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP  
GIRPYLATLAGNFRMPVPLREYLMGGICPVSRDTIDYLLSKNGSGNAIIIVVGAAESLSM  
PGKNAVTLNRNKGFKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRWVQKKFKYIGFA  
PCIFHGRGLFSSDTWGLVPYSPKITTVVGEPIITIPKLEHPTQQDIDLYHTMYMEALVKLFDK  
HKTKEGLPETEVLEVN

**Important features of the protein:****Transmembrane domain:**

amino acids 76-97

**N-glycosylation sites.**

amino acids 60-63, 173-176, 228-231

**N-myristoylation sites.**

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

**FIGURE 165**

GGGCGGCGGGATGGGGGCGGGGGCGGGGGCGCCGCACTCGCTGAGGCCCCGACGCAGGGCCGGGCGGGCCCA  
 GGGCCGAGGAGCGCGGCGGCCAGAGCGGGGCGGGAGGCGACGCCGGGACGCCCGCGCGACGAGCAGGTGGCG  
 GCGGCTGCAGGCTTGTCCAGCCGGAAGCCCTGAGGGCAGCTGTTCCCACTGGCTCTGCTGACCTTTTGCTTTGGA  
 CGGCTGTCTCAGCGAGGGGCGTGCACCCGCTCTGTAGCAGCGCCATGGGGCTGTGGCCCTTCTTGAAGACCCA  
 CTGCTGTGCACTGCTGGTGGCTTTGTCTTCGTGTGAGTGTCTTGGTCATCAACTTCGTCCAGCTGTGCAC  
 GCTGGCGCTCTGGCCGCTCAGCAAGCAGCTCTACCGCCGCTCAACTGCCGCTCGCTTACTACTCTGGAGCCA  
 ACTGTCATGCTGCTGAGTGGTGGTCTGCACGGAGTGTACACTGTTACGGACACGGCCAGGTAGAGCGCTT  
 TGGGAAGGAGCAGCAGTCATCATCTCAACCACAACCTCGAGATCGACTTCCCTGTGGTGGGACCATGTGTGA  
 GCGCTTCGGAGTGCTGGGAGCTCCAAGTCTCTGCTAAGAAGGAGCTGCTCTACGTGCCCTCATCGGTGGAC  
 GTGGTACTTTCTGGAGATTGTGTTCTGCAAGCGGAAGTGGGAGGAGACCAGGACACCGTGGTGAAGGCTGAG  
 GCGCTGTGCGACTACCCGAGTACATGTGGTTCTCTGTACTGGAGGGGACGCGCTTACGGAGACCAAGCA  
 CCGCGTTAGCATGGAGGTGGCGGCTGTAAAGGGCTTCTGTCTCAAGTACCACCTGCTGCCCGGACCAAGG  
 CTTCAACCCGAGTCAAGTGCTCCGGGGGACAGTCGAGCTGTCTATGTAACCTGAACTTCAGAGGAAA  
 CAAGAACCCGCTCTGCTGGGATCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCCTCT  
 GGAAGACATCCCGCTGGATGAAAGGAAGCAGCTCAGTGGCTTCATAAATGTACCAGGAGAGGACGCGCTCCA  
 GGAGATATATAATCAGAAGGCATGTTCCAGGGGAGCAGTTAAGCTGCCCGAGGCGCTGGACCCCTCTGAA  
 CTTCTGTCTGGGCCACCATTTCTCTGTCTCCCCCTCTCAGTTTGTCTTGGCGTCTTTGCCAGCGGATCACC  
 TCTCTGATCTCCTTTCTGGGGTTGTGGGAGCAGCTTCTTTGAGTGTGCAGATGATAGGAGAACTGCT  
 TGAACCTGGGAGGTGGAGATTGCAGTGAGCTGAGATGGCATCACTGTACTCCAGCTAGGCAACAGAGCAAGACT  
 CAGTCTCAAAAAAAAAAAAAACAAAAACCCAGAAATCTGGAGTTGAACCTGTGTAGTTACTGACATGAAA  
 ATTCATAGAGGCTGAACAGCAGATTTGAGCAGGCAGAAAAAATCAGCAAGCTGAAGATGGTACCTTGAGATT  
 TTTCAAGCTAATGAAAAAGAAATGAAGAAAAATTAACAGCTCAGAGACCATGGTGCACCTGACACAAATCAA  
 CATATGCATGATGAGAGTCCAGAAAGGAGAGGAGAGAAAGGTCAGAAAGATGGCCACAAGCTGATGAAAAACA  
 GTAACCTACCCTCAGGAAGCTCAGTGAACCTCAATGAGATGAATATCAGAGATCCACACCTAGATATTTCTAT  
 AATCAAAGTCAAAATGACAAAGAACTTTGAAAGCAGCAAGAGATGAGCAACTATCTTGTTCAAAGGATCTTTG  
 ATCAGATTGAACAGCTCATTTCTCTCAGAAATCATGGGAGCCAGGAGATGCGGATGAACACTGTTGAAGGCAA  
 AACCTCAACTGTAATTATTGGACTTTTGTGCTTAGATGGCTCTGACTCTTTGTCTTCAGGAGGCTTTTCA  
 ATTTAATCCCTAATAACAATTAGTCAAGCTTCTTGTGACTGTAGGAAGGCTGTCTTTAGGCCGGGCACAGTGGC  
 TTACACCTGTAATCCAGCACTTTGGGAGGCCAGACGGGTGGATATTGGGTCAGGCTGATCTCAAACCTCT  
 GAGTTTCAGGTGATCTGCCGCCCTCAGCCTCCCAAAGTGTGTGATTGCAAGGCGTGAGCCACTGCCCTGGCCGA  
 ATTTCTTTTAAAGCTGAATGATGGGGCCAGGCACGATGGCTCAGCCTGTGATCCCAAGTAGACTTGGATTGTA  
 AACATGCACCCACCATGCTGGCTAATTTTTGTATTTTTAGTAGAGACGTGTAGCCAGGCTGGTCTCGATCTCCT  
 GACCTCAAGTGACCACTGCTCAGCCTCCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTGCTGGCCTTGA  
 GCATCTTGTGATGTGCTTATTGGCATTGTATATCTCTATCTTTGGGGAATGTCTGTCAAGTCCCTTTG  
 CCTTTTTAAATTTTTATTATTTATTTATTTATTTATTTTGGAGACAGGCTCTGTCTGTGTCAGGCTGGAGTA  
 CAGTGCACAGTCTGGCCCACTCAGCCTCAGCCTCCTGGGCTGAGTGATCTCCCACTCAGCCTGCCCTGTG  
 AGCTGTATTTTTTGTATTTTGTATTTTGTAGCTGTAGTTTTTGTATTTTTTGTGGAGACAGCATTTACCATGA  
 TGCCAGGCTGTGCTTGAACCTCTGAGCTCAAGTGTATCTGCTGCTTCAAGCTCCAAAGTGTGGGATTACAGA  
 CATGAGCCATGCACCTGGCAAACTCCCAAAATTAACACACACACAAAAAACCACTGATTCAAAATGGGCA  
 GAGGGCCGGGTGTGGCCCAACTACCAAGGAGACTGAAGTGGGAGGATCGCTTGGGATGAGAGTCTGAGGCTG  
 CAGTGAGTCGAGGTGTGCGCATGCATTCCAGCCTGGACAACAGAGTGAAGCCTGTCTC

**FIGURE 166**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVG FVFVVSGLVIN FVQLCTLALWPVSKQLYRR LNCRLAYSLWSQLV
MLLEWWSCTECTLF TDQATVERFGKEHAVI ILNHNFEIDFLCGWTMCERF GVLGSSKVLAKK
ELLYVPLIGWTWYFLEIV FCKRKWEEDRDTVVEGLRRLSDY PEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVT LNFGRGNKNPSLLGILYGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQE IYNQKGMFPGEQFKPARRPWTL LN
FLSWATILLSPLFSFVLGVFASGSPLLIITFLG FVGAASFGVRRRLIGESLEPGRWRLQ
```

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 307-323, 335-352

**Tyrosine kinase phosphorylation sites.**

amino acids 160-168, 161-169



**FIGURE 167**

GATATTCTTTATTTTTAAGAATCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGGCA  
 GCCACCAGGCATATTCATCTTTGTGTGTGTTTTCTTTTGCTTTAGCACTGGGGCACTTCTT  
 GCTTATTTCTTTGGTAGGAAAGGGGCTCAGTTTGTCTTGTGGGGTGGTGGCAGGCAGGCCG  
 GCTTACGCCCTGATACGGCCCTGGGTTAGAAGGGAAGGAAGATAAACTTTTATACAAATGGG  
 GATAGCTGGGGTCTGAGACCTGCTTCCTCAGTAAATTCCTGGGATCTGCCTATACCTTCTT  
 TTCTCTAACCTGGCATACCCTGCTTAAAGCCTCTCAGGGCTTCTCTCTGTCTTAGGATCAA  
 AGTATTTAGAGCTACAAGAGCCCTCATGGTCTGGCCCCCTGCCCCCTGGCCAGCTTCATTGT  
 ACATGTGGTGTCTCTTGTCTCCTG**TAA**TGTGGTATGCCATGGGGTCTTTGCACAAGCCT  
 TTCCTCTTTGGCTGGACACTGTTCCTGCCCCCCCCATACCTCTTCTACTTAATATGTAGTC  
 ATCCTGCAGATTTCAATTCTAACATCATTTTTCTCCAGGGATCCTGGCCTGACAGAATCTCAT  
 CTTGTTTAATGCTCTCATAAGACCACTTGTTTCCCTTTTGCAGCACTTGCCACTCAGTTGTA  
 TCTTTATGTGCGTTTGTGGTTGTATGGGTGTGTCTGTTCCCCAGAATGCCAGCTCTGAGC  
 TGCGTGAGGGTCAAGGGCATTGCTGTGCTGCCAGGTATAGTGCTTACATGTGGTGGTGCT  
 CATGTTTTAGAGACTAAATGGAGGAGAGATGAGGAAAAGATTGAAATCTCTCAGTTACCA  
 GATGGTGTAGGGCCAGCATTGTAAATTACACGTTGACTGTGCTTGTGAATTATCTGGGGA  
 TGCAGGTCTTGATTCAAGTAGGCCAGGTTGGGCATCTCTAACAACTCCACGTGATGCTGA  
 TGCTGGTCTATGAACATACTAAATAGTAAGAATCTATGGAGCCAGGCTGGGCATGGTGCC  
 TCACACCTATGATCCAGCACTTTGGGAGGCTGAGGCAGGCTGATCACCTGGAGTCAGGATT  
 TCAAGACTAGCCTGGCCAACATGGTGGAAACCCATCTGTACTAAAAATACACAAATTAGCTG  
 GGCATGGTGGCACATGCCTGTAGTCCCAGCTACTTGGGAGGCTGAAGCAAGAGAATCGCTTG  
 AACCTGGGAGGCGGAGGTTGCAGTGAGCCGAGATCAGGCCACTGTATTCCAACAGGGTGAC  
 AGAGTGAGACTCTATGTCCAAAAAAAAAAAAA

**FIGURE 168**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSLQCPGAATRHILCVCFSAIALGHFLLISLVGKGLSLSCGVGGRQAGLRLIRPWVRR
EGKINFYTNNGDSWGLRPASSVKFLGSAYTFFSLTWHITLLKASQGFSLFLGSKYLELQEPSWS
GPCPPGQLHCTCGVLLSFL
```

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**FIGURE 169**

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA  
TTATAGGTGTAAGCCACCGTGTCTGGCCTCTGAACAACCTTTTTCAGCAACTAAAAAGCCAC  
AGGAGTTGAACTGCTAGGATTCTGACTATGCTGTGGTGGCTAGTGCTCCTACTCCTACCTAC  
ATTAAATCTGTTTTTTGTCTCTTGTAAGTACGCTTTACCTTCCTAACACAGAGGATCTGT  
CACTGTGGCTCTGGCCCAAACCTGACCTTCACTCTGGAACGAGAACAGAGGTTTCTACCCAC  
ACCGTCCCTCGAAGCGGGGACAGCCTCACCTTGCTGGCCTCTCGCTGGAGCAGTGCCCTC  
ACCAACTGTCTCAGCTCTGGAGGCACTGACTCGGGCAGTGCAAGGTAGCTGAGCCTCTTGTTA  
GCTGCGGCTTTCAAGGTGGGCCTTGCCCTGGCCGTAGAAGGGATTGACAAGCCCGAAGATT  
CATAGGCGATGGCTCCCACTGCCAGGCATCAGCCTTGCTGTAGTCAATCACTGCCCTGGGG  
CCAGGACGGGCCGTGGACACCTGCTCAGAAGCAGTGGGTGAGACATCACGCTGCCCGCCCAT  
CTAACCTTTTCATGTCCTGCACATCACCTGATCCATGGGCTAATCTGAACTCTGTCCCAAGG  
AACCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAAGGGGTCTGCTTAGACCACCTGGTT  
TATGTGACAGGACTTGCATTCTCTGGAACATGAGGGAACGCCGAGGAAAGCAAAGTGGCA  
GGGAAGGAACCTTGCCAAATTATGGGTCAGAAAAGATGGAGGTGTTGGGTTATCACAAGGC  
ATCGAGTCTCCTGCATTGAGTGACATGTGGGGGAAGGGCTGCCGATGGCGCATGACACACT  
CGGGACTCACCTCTGGGGCCATCAGACAGCCGTTTCGCCCCGATCCACGTACCAGTGCTG  
AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAAATCTGCGATCACCAG  
CCAGGGGCAGCCGTCTGGGAAGGAGCAAGCAAAGTGACCATTCTCCTCCCCTCCTTCCCTC  
TGAGAGGCCCTCCTATGTCCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGGCTAATG  
GCTCAGTGTTGGCCAGGAGGTGAGCAAGGCCTGAGAGCTGATCAGAAGGGCCTGCTGTGCG  
AACACGGAAATGCCTCCAGTAAGCACAGGCTGCAAAATCCCAGGCAAAGGACTGTGTGGCT  
CAATTTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT  
TCAAATGATCTCCAAGGGCCCTTATACCCAGGAGACTTTGATTTGAATTGAAACCCCAA  
TCCAACCTAAGAACCAGGTGCATTAAAGAATCAGTTATTGCGGGGTGTGGTGGCCTGTAATG  
CCAACATTTTGGGAGGCCGAGGCGGGTAGATCACCTGAGGTGAGGAGTTCAAGACCAGCCTG  
GCCAACATGGTGAAACCCCTGTCTCTACTAAAAATACAAAAAACTAGCCAGGCATGGTGGT  
GTGTGCCTGTATCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT  
GAAGGAGGCTGAGACAGGAGAATCACTTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA  
AAAAATAAAAAAGAATTATGGTTATTTGTAA

**FIGURE 170**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLEALTRAVQVAEPLGSCGFQGGPCPGRRRD
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**Signal peptide:**

amino acids 1-15

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**FIGURE 171**

GCGGGCCCGCGAGTCCGAGACCTGTCCCAGGAGCTCCAGCTCACGTGACCTGTCACTGCCTC  
 CCGCCGCCTCCTGCCCCGCCATGACCCAGCCGGTGCCCCGGCTCTCCGTGCCCGCCGCGCT  
 GGCCCTGGGCTCAGCCGCACTGGGCGCCGCTTCGCCACTGGCCTCTTCCTGGGGAGGCGGT  
 GCCCCCATGGCGAGGCCGCGAGAGCAGTGCTGCTTCCCCCGAGGACAGCCGCTGTGG  
 CAGTATCTTCTGAGCCGCTCCATGCGGGAGCACCCGGCGCTGCGAAGCCTGAGGCTGCTGAC  
 CCTGGAGCAGCCGCAGGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTTGGCCAACC  
 TGGCGCGGCTCATCCAGGCCAAGAAGGCGCTGGACCTGGGGACCTTCACGGGGTACTCCGCC  
 CTGGCCCTGGCCCTGGCGCTGCCCGCGGACGGGCGCTGGTGACCTGCGAGGTGGACGCGCA  
 GCCCCCGGAGCTGGGACGCCCCCTGTGGAGGCAAGCCGAGGCGGAGCACAAGATCGACCTCC  
 GGCTGAAGCCCGCCTTGGAGACCCCTGGACGAGCTGCTGGCGGCGGGCGAGGCCGCGCACCTTC  
 GACGTGGCCGTGGTGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA  
 GCTGCTGCGACCCGAGGCATCCTCGCCGTCTCAGAGTCTGTGGCGCGGGAAGGTGCTGC  
 AACCTCCGAAAGGGACGTGGCGCCGAGTGTGTGCGAAACCTAAACGAACGCATCCGGCGG  
 GACGTGAGGGTCTACATCAGCCTCCTGCCCTGGGCGATGGAATCACCTTGGCCTTCAAGAT  
CTAGGGCTGGCCCCTAGTGAGTGGGCTCGAGGGAGGGTTGCCTGGGAACCCAGGAATTGAC  
 CCTGAGTTTAAATTGAAAATAAAAGTGGGGCTGGGACACAAAAAAAAAAAAAAAAAAAA

**FIGURE 172**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282  
><subunit 1 of 1, 262 aa, 1 stop  
><MW: 28809, pI: 8.80, NX(S/T): 1  
MTQFPVRLSVPAALALGSAALGAATGLFLGRRCPPWRGRREQCLLPEDSRLWQYLLSR  
MREHPALRSRLRLTLEQPGDSMMTCEQAQLLANLARLIQAKKALDLGTFTGYSSALALAL  
PADGRVVTCEVDAQPPELGRPLWRQAEAEHKIDLRRLKPAETLDELLAAGEAGTFDVAVVDA  
DKENC SAYYERCLQLLRPGGILAVLRVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS  
LLPLGDGLTLAFKI

**Important features of the protein:****Signal peptide:**

amino acids 1-25

**Transmembrane domains:**

amino acids 8-30, 109-130

**N-glycosylation site.**

amino acids 190-193

**Tyrosine kinase phosphorylation site.**

amino acids 238-246

**N-myristoylation sites.**

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

**Amidation sites.**

amino acids 31-34, 39-42

[illegible]

**FIGURE 174**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286  
><subunit 1 of 1, 671 aa, 1 stop  
><MW: 74317, pI: 7.61, NX(S/T): 0  
MPHAFKPGDLVFAKMGYPHWPARIDDIADGAVKPPPNKYPIFFFGTHETAFLGPKDLFPYD  
KCKDKYKGPNKRKGFNEGLWEIQNNPHASYSAPPPVSSSDSEAPEANPADGSDADEDDDRG  
VMAVTAVTATAASDRMESDSDSKSSDNSGLKRKTPALKMSVSKRARKASSDLDQASVSPSE  
EENSESSSESEKTSQDFTPEKKA AVRAPRRGRLGGRKKKKAPSASDSDSKADSDGAKPEPV  
AMARASASSSSSSSSSDSVSKKPPRGRKPAEKPLPKPRGRKPKPERPPSSSSSDSDSDEV  
DRISEWKRRDEARRRELEARRRREQEEELRRLREQEKEEKERRRERADRGEAERGSGGSSGD  
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEAREAKSAKPKQSSSTEPARKPGQKEKRV  
RPEEKQQA KPVKVERTKRSEGFMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDS PDVKRC  
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMKAAEVYTRLKSRVLGPKIEAV  
QKVNKAGMEKEKAEKLAGELAGEEAPQEKAEDKPDSTDLAPVNGEATSQKGESAEDEKEHE  
EGRDSEEGPRCGSSEDLHDSVREGPDLDPRPGSDRQERERARGDSEALDEES

**Signal peptide:**

amino acids 1-13



# FIGURE 175

GTTGGTCTCTCGGTGATCTTCACCTTTACCAACTGCAGATCTTGGGACTCATCAGCCTCAATAATTATATATAAATTA  
 ACACCATTTTGAAGAGAGCAATTGTTTTATCATCTAGTAAGTCTAATAAAGATGAAGAAGCTTAAAGCCAGAGCCAGGA  
 TTTTCACTTTTCTGCTTTTGTATGATGCTAAGCATGACCATGTGTCTTCTTCAGTCTACTGGCCACTTTGAACCA  
 AATATTCCAAGACTCAAGCTAACCTACAAAGACTTGTGCTTTCAAATAGCTGATTTCCCTTTTGGGTTTCATC  
 AGAAGGACTGGATTTTCAAATCTCTTCTTCTAGATGAGGAAGAGGAGGCTGTCTTGTGGAGGCCAAAGACCAT  
 CTTTCTACTAGTCTGGTGAAGCTTAAACAAAATTTAAGAAGATTTATTCAGAGTACTTCAAGCCTATTAACAA  
 AACTCACATATATGTGTGTGAAGCTGGAGCATTTTCATCCAATATGTGGGTATATGATCTTGGAGTCTACAGGA  
 GGATATTATATTCAAATAGACACATAAATTTGGAGTCTGGCAGACTGAAATGTCTTTTCGATCCTCAGCAGCC  
 TTTTGGCTTCAGTAATGACAGATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCCCTGGCAAAGATACTGCAT  
 CACTCGATCCCTTGGGCCCTACTCATGACCACCACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG  
 AGCAAAATTTATTTGGAACCTTCTTATACAGACACCACTACAATCCAGATGATGATAAAATATATTTCTCTTCTCG  
 TGAATCATCTCAAGAAGGCAGTACCTCCGATAAAACCATCTTCTCAGTGTGGAAGAGTTTGTAAAGATGATGT  
 AGGAGGACACAGCAGCCTGATAAACAGTGGACGACTTTCTTAAAGCCAGACTGATTTGCTCAATTCCTGGAAG  
 TGATGGGGCAGATACTTACTTTGATGAGCTTCAAGATTTTATTACTCCCCCAAGAGATGAAGAAGATCCTGT  
 AGTATATGGAGTCTTTACTACAACAGCTCCATCTTCAAAGGCTCTGTGTTTGTGTATAGCATGGCTGACAT  
 CAGAGCATTTTAAATGGTCCATATGCTCATAAGGAAGTGCAGACCACTCGTGGTGCAGATGATGGGGAAT  
 TCCCTTATCCACGGCTGCTACATGTTCCAAAGCAAACTATGAGCCACTGATTAAGCTCCACCGAGATTTTCCAGA  
 TGATGTACATGCTTTCATAAGCGGCACCTCTGTGATGTATAAGTCCGATTAACAGTTCGAGGAGGACCAAGCTT  
 CAGAAGATCAATGTGATATACAGCTGACACAGATAGTGGTGGATGATGTCATTCGAGAAGATGGCCAGTACGA  
 TCTAATGTTTCTTGGACACAGACTTGGAACTGTCTCAAAGTTGCTCAGCAATTCAAAGGAAGTGGAAATATGGA  
 AGAGCTAGTGTGGAGAGTTCGAGATATTAAGCACTCATCAATCATCTTGAACATGGAAATGTCTCTGAAGCA  
 GCAACAATTGCACTTCTGCTTCCCGAGATGGATTTGCTCAGCTCTCCTTGCAGATGGCACTTATGGGAAGC  
 TTGCGCAGACTGTCTCTTGGCAGAGACCCCTACTGTGCTGGGATGGAAATGCATGCTCTCGATATGCTCTTAC  
 CTCTTAAGAGGAGAGCTAGACGGCCAGATGTAATAATGGGCAACCAATCAGCAGTCTGCGGACATGCAGACAG  
 CATTAGTCTGAACCTGCTGATGAAGAGTGATTTTGGCATTGAAATTTAACTCAACCTTTCTGGAATGTATACC  
 TAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTCAGGGGATGAGCATCGAGAGGAGTTGAAGCCCGA  
 TGAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAGTTTGCAGAAGAGGATTCGGGATGTATTACTG  
 CAAAGCCAGGAGACACTTTTCATCCACCACTAGTGAAGCTGACTTTGAAATGTCATTGAGAAATGAACAGATGGA  
 AAATACCCAGAGGGCAGAGCATGAGGAGGGGCAGGTCAGGATCTATTGCTGAGTCAGGTTGAGATCAAAAGA  
 CTACATCCAAATCCTTAGCAGCCCAAATCTCAGCCTCAGCCAGTACTGCGAACAGATGTGGCCACAGGGAAGCG  
 GAGACAGAGAACAAGGGGGGCCAAAGTGGAAAGCATGCAGGAAATGAAGAAGAAACGAAATCGAAGACATCA  
 CAGAGACCTGGATGAGCTCCCTAGAGCTGTAGCCACGTAGTTTCTACTTAAATTAAGAAAAAGAAATTCCTTACC  
 TATAAAAAATTTGCTCTCTGTATATATCCCTTATAGTAATTCATAAATGCTTCCCATGGAGTTTGTGCTAAGG  
 CACAGACAATAATCTGAATAAGACAATATGTGATGAATATAAGAAAGGGCAAAAAATTCATTTGAACAGTTTT  
 CCAAGAACAATCTTGCAAGCAAAATATAAGAAATATCCTAAAAATAGGGGGTTTACAGTTGTAAATGTTTTA  
 TGTTTTGAGTTTTGGAATTTATTTGTCATGTAATAGTTGAGCTAAGCAAGCCCGGAATTTGATAGTGATATAAGGT  
 GCTTTTTCCTCGAATGTATCTTAAAGCATGGAATTTACCATTGCACTGTGCTATGTTCTTATGAACAGATATAT  
 CATTTCTTATGAAGAACAGCTACCTTTGTGGTAGGGAATAAGAGTGCAGACAAATTAAGACAACCTCCCATATTC  
 AACAGAACTTTCTCAGTGAGCCATCTACTCTGGAGAAATGGTATAGAAATTTGGAGAGGTGCATTTTCTTCT  
 TGGCCACTGGGGTTAAATTTAGTGTACTACAACATTTGATTTACTGAAGGGCACTAAATGTTTCCCCAGGATTTCT  
 ATTGACTAGTCAGGAGTAAACAGGTTTCAGAGAGAGAAGTTGGTGTCTGTTATTATGTATATATACTAA  
 GCTCTCAGGGACAGATGCTTAAATAATACTTTAATAAGATATGGGAAAAATTTTAAATAAAACAGGAAACA  
 TATAAGTGTAAATGCATCTGATGGGAAGGCATGCAGATGGATTTGTAGAGACAGAGGAAACAGAGCCAT  
 AAATTTCTGGCTTTGGGGAACATCTATCCCATGAAGGAAGGAACAATCACAAATAAGTGAGAGTAAATGTAA  
 TGGAGCTCTTTTCACTGAGTTTAAAGTACGTGCCAATTTGTAATTCATCTGTAAAAAAATCTAGATATAACA  
 AACTGCTAGCAAAATCTGAGGAACATAAATTTCTTGAAGAATCATAGGAAGAGTAGACATTTTATTTATAAC  
 AATGATATTCAGTATATATTTTCTCTTTTAAAAAATATTTATCATCTGTATATATTTCTTTTACTGTC  
 CTCTTATCTCTCTGTATATTTGGATTTTGTGATATATTTGAGTGAATAGGGAACACATATATAACACACAGA  
 GAAATGAAGAATGACATTTCTGGGAGTGGGATATATATTTGTTGAATACAGAACGAGTGTAAATTTTAAAC  
 AACGGAAGGGTTAAATTTAACTCTTTGACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAAT  
 GTAGTATTGTTTTGTAATTTAAACAATAAAGCCTGCTACATGT

**FIGURE 176**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNI PRLKLT YKDLLLSNSCIPFL
GSSEGLDFQTL LLLDEERGRLLL GAKDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLGPTHDHHYIRT DISEHYWLN GAKFIGTFF
IPDTYNPDDDKIYFF FRESSQEGSTSDKTI LSRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSV MYKSVPV
AGGPTFKRINVDYRLTQIVVDHVIAEDGQYDVMFLGTDIGTVLKVVSISKEKWNMEEVVLEE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCLARDPYCAWDGNA
CSRYAPT SKRRARRQDVKYGDPITQCWDIEDSISHETADEKVI FGIEFNSTFLECI PKSQQA
TIKWYIQRSGDEHREELKPD ERIIKTEYGLLIRSLQKKDSGMYCYCAQEHTFIHTIVKLT LN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKKRNRRHHRDLDELPRAVAT

```

**Important features of the protein:****Signal peptide:**

amino acids 1-36

**N-glycosylation sites.**

amino acids 139-142, 607-610, 724-727

**Tyrosine kinase phosphorylation site.**

amino acids 571-576

**Gram-positive cocci surface proteins 'anchoring' hexapeptide.**

amino acids 32-37

# FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCCGCAGAGGTCATCCTGGAGCATGCCACCGGGGAGCAGA  
 CACCTCCCCAGGTAAAGCTGGGAGCAGACCTGAAGCTGTTCTTCCAGGAGCTGGTGATTTTCCCCACCCAC  
 CTACAGAGTTTACAGCCAGGAGGACTGATCAGGTGTGTCTCGGAGTGGGGAGCAGAAAGGCGTGGCTGGCAGA  
 GTGGCTGGAGAAAGAGGTTTACGCGCTTGACCAAGCCGAGCTGCCCTGACTACAAAGATCCAGAACCTTGGGATC  
 GGGTGAGGTGGGGGGGACAGGTGTCTGTGCACTTCTTGTCTCAGCAAGAACAGCTGAGAGAGGGGATCTTGG  
 AGCCATTAGGGGTGCTATGGAGCTACAGAGGGGAGGGAAGGTATTTTAAGGTAAACAGTGTGGCACAATAGTTAA  
 GAGCACAGTTTTTGGAGCTAGACCCACATAGGTTCAAATTTCTCTTCTGTGCTTCTTCTAGTTCTGTAGTCCCGAGGT  
 AAGGAGTGACTTAACCTCTCTGGACTTCAATTTCTCTCATCACTAAAGTAGGGCCAAATAAGCACCCACTCAT  
 AAGGAAGATTAAATGACATAATGTATGTGATGCACTGCAACTAGCAAAAGTACCACTAGTAAGCTCATGCCCCACAG  
 TATTTCCACCCACCCCTGTTCTCTGCTTCCCAACCAAGGTACTGCAACAGCTGGAGCAGAGGGCGCAGCAGGCTT  
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTTACAGGAAGTGCAGAGAGCATCCGCGGGGACAGGTGAGCC  
 AGGTGAAGGGGGCTGCCCGCTGGCCCTGCTGCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA  
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGCGGCTCAGTGAGGCTCGGCTGTCCAGAGGGACCTCTCTC  
 CAACCGCTGAGGATGCTGAGCTTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTTGAGGAGCTGCC  
 CCCAAGCCCTGGCCACGAGGGCCCTCCCTGCCCTGCACAGTGTATTTTCGCTATCAGGACGGCGTGAGGATG  
 AGCTGACAATCACGGAGGTTGAGTGGCTGGAGTGCATAGAGGAGGAGATGCTGACGAATGGGTCAAGGCTCGGA  
 ACCAGCACGGCGAGGTAGGCTTTGCTCCCTGAGCGATATCTCACTTCCCGGACCTCTCCCTCCAGAGAGCAGCC  
 AAGCAGTGACAAATCCCTGCGGGGACAGCCACAGCATTTCTGGCAGCAGCCGTGACAGTACACGGGACAGA  
 GTGACAGAGCTGAGCTTCCCTGAGGGGCACTACCTGCTGCCCGGGCCAGAGTGGAGTAGATGAGG  
 GCTTTGAGGGGAGAAATTTGGGGCCGCTGTGGGCTCTCCCTCGCTGCTGGTGAGAGAGCTGCTTGGCCCC  
 CAGGGCCACTGAATCTTGACCTTGAACAGATGCTGCCGTCCCTCTCTCCAGCTTCTCCCAAGCTGCAC  
 CTACCTCTGTGTGGTGGCCCCCTGCACCTGTCTGCTGGGGACAAAGCCCTGAGCTTCCCTGGGTCTCTGG  
 ACATGTGGCGACCTCCAGCTCAGGCGGATGCTGCCACCTCCCGCGCGCTGAAGCTTCCCTGCTGCTGG  
 CAGATCCCTCATCCTGAGGCGAAGCCCTTGAACCCCACTCCTTTTTCCTCATTTGTTATCATCTCTAGGAC  
 GGAATCTACTACCTTCTCTCTGATGACCTATCTAGGTTGGTGAATGCTGAAATCTCTGGGGCTGGAAACC  
 ATCCATCAAGGCTCTAGTAGTTCTGGCCCCACTTTCCCACTCCCTGGCTGCATGACCCCACTCTGGATG  
 CCAGGCTCACTGGGTGGGCTGGGGAGAGGAACAGGCTTGGGAATCAGGAGCTGGAGCCAGGATGCGAAGCAG  
 CTGTAATGGTCTGACGGGATTTATTGACAATGAATAAAGGGCAGAGGCCAGGCCAGGGCTGGGCTCTTGTG  
 CTAAGAGGCGAGGGGGCTACGGTGCTATTGCTTTAGGGGCCACACAGGGCAGGGGCTGCTCCAGCTGCCAC  
 GCTCTATCATATGGAGCAGAGTGTGGGGAAGGCGGGCAGGACGCTGTGCAAGGCGAGGGAAGGAGAAGAC  
 TGAGGGGCTGTGACCTCTCTGAGGCCCCAGCCTGAGACTGTGCAACTCCAGGCTGGAAGTAGAGCTGTGCTCT  
 AGCTGGGGGCGAGTGTCTGCTGAGGGGAGGGCTTTCACGCCACCCAGCCCTGGGCTGCCAGCTGGTAG  
 TCCATCAGCACAATGAAGGAGACTTGGAGAGAGGAAGAAATAACACTGTTGCTTCTGTTCAAGCTGTGTCAGC  
 TTTTCCCGTGGGCTCCAGGACCTTCCCTACCTCCACACCAAAACCAAGGATTATAGCAAAAGGCTAAGCCCTGC  
 AGTTTACTCTGGGGTTTCAGGAGCGCAAGGCTTAATAGTTTAAAGTAGGTGATGGGAAGATGAGATTACCTCA  
 TTTAGGCTCAGGACAGCTCACTACATACATACCTCCCTGCTCCCTGTGGTAGAGACACTGAGAGAAAGGGGAGGG  
 TCAACAATGAGAGACAGGAGTAGTCTATCAGTGCCCGCCAGATAGAGAGCAATAGAGGCCACCGCCAGTGC  
 AGTCCCGGCTGTGTTTCTTCTACCTGCTGATCAGAAGTGTCTGGTTGCTGGCTTTCCTTGGCTTCTGATGG  
 CGAGCCCTGGGCTTGGGCCCTCCCTCCGCGCTCAGTGTTGGCTCTGCAGAAGCTCTGGGGTTCCTTCAAGTG  
 CACAGGGGTAGGCTGTGCTCCCTGAGTCTCTCATTTGTGATGGGGGCTAGGCTGAGGAGCTGGGCTGGGCC  
 TGTCAAGGGGACGCTCTCATAGGAGGATCCTGCTGCTGGGCTGCCCTCCCGAGACCCCTGACCAACCCCTG  
 GCTCTTCTCCCAACAGAGGCCAGCTCCTGCTGTGGGGAGGAGGATCAGGCTGCTGCTGAGCTGATAGGCTTCTC  
 TCTCAATGTGTGTCACCCGAACCTGGGAGGGGAGGAGACACTGGGTTTAGGACACAACTCAGAGGCTGCTGT  
 GCCCTCCCTCTGACCAAGGACATCTGAGTTTGGTGGCTACTTCCCTCTGCGCTAAGGTAGGGGAGGCTTCTC  
 AGATTGTGGGACATATTGCTAGCTGACTTCTGCTGAGCTCCGATCCAGGAGGAAGAGGCCAAGGCCACTT  
 TTTGGATGAGGCTGATCATGACTGGCCCCCTACCTCAGCCCCCTTCCCTGAGACACTGCCCACTGCCCA  
 CAGAGAACAGTGGCTTCCCTGTCCGGGGCGGCTTTTCTCTTCTTGGAGCTCCCTGACGGCAAGTGGAG  
 GCTCTTCTGCTGGGCTGCAATGATGCGAAGGGCTCAGAGGACAGGCTGATGTGATGATGGAGGGGCTC  
 CGTCTGCAGGCTGAGCTGCATACACACTGACAGCAGGAGAGGGAGTGAAGGTAACTTTCTCATTTCCCT  
 TCTATGTTTGTCTTACGTTCTTTCAGCAIGCTCCTTAAACCCCAAGAGCCCAATTTTCCCAAGCCCAATTT  
 TTTCTGTCTTATCTAATAAATCAATTAAG

**FIGURE 178**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFVRYQAGREDELTTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESQSDSDNPGCAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDDGFWRGEFGGRVGVFPSSLVEELLGPPGPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPPAKAPDPGHPDPLT
```

## FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGAGAAAGAGACAGAGACAAGGCCACAGCGGAA  
 GAGGGCAGAGACAGGGCAGGCACAGAGCGGGCCACAGACAGAGTCTCTACAGAGGACAGGCACAGAGAGCTGCAGA  
 AGACACAGGCAGGAGAGACAAAGATCCAGGAAAGAGGGCTCAGGAGGAGAGTTTGGAGAGACAGACCCCTGG  
 GCACCTCTCCCAAGGCCAAGGACTAAGTTTCTCCATTTCCTTTAACGGTCTCCAGCCCTCTGTAAGAACTTTGGC  
 TCTGACTTTGGCAGAGTCCAAAGCCCCAGGCTACAGAGAGAGCTTTCCAAAGCTAGGGTGTGGAGGACTTGGT  
 GCCTTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAGTGGC**ATGT**CCACAGACAGGCTCGCATCCCGGGAGGGG  
 CTGGAGAGGCGCTGGCTGTGGGGAGGCCAACCTGCCCTCCTGCTCCCATTTGTGCCCTTCTGTGGCTGTGTGT  
 GCTGCTTCTGCTACTGCTGGCTCTCTCCTGCCCTCAGCCCGGCTGGCCAGCCCTCTCCCCGGAGGAGAGAT  
 GGTGTTTCCAGAGAGATCAACGGCAGCGTCTGCTGCTGGCTGGCGCCCTGCCAGGCTGTTGTGCCCTTGTGA  
 GGCTTTGGGGAGACGCTGCTACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTGCAGGGGCTGACAGTGCAGTA  
 CCTGGGCCAGGCGCTGAGCTGCTGGGTGGAGCAGAGCCTGGCACCTACCTGACTGGCACCATCAATGGAGATCC  
 GGAGTCGGTGGCATCTCTGCATGGGATGGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACCTCCA  
 CCTCCAGCCCCGTGGAGGAGGCCACCCCTAACTCTGCTGGGGACCTGGGGCTCACATCCTACGCCGAAGAGTCC  
 TGGCAGCGGTCAAGTCCCATTGTGCAACGTCAAGGCTCCTCTTGAAGACCCAGCCACAGACCCCGAAGAGCCAA  
 GCGCTTTGCTTCACTGAGTAGATTTGTGGAGACACTGGTGTGGCAGATGACAAGATGGCCGATTCCACGGTGC  
 GGGGCTAAAGCGCTACCTGCTAAAGTAGTGGCAGCAGCAGCCAAAGGCTTCAAGACCCCAAGCATCCGCAATCC  
 TGTCACTTGGTGGTGACTCGGCTAGTGATCCTGGGTTCAGGCGAGGAGGGGGCCAAAGTGGGGCCAGTGGCTGC  
 CCAGACCTTGGCAGCTTCTGCTGCCCTGGCAGCGGGGCCCTCAACACCCCTAGGAGACTGGGGCCCTGACCATTGGA  
 CACAGCCATTCTGTTTACCGTCAGGACCTGTGTGGAGTCTCACTGCGACAGCTGGGATGGCTGATGTGGG  
 CAGCCCTGTGACCCGGCTCGAGCTGTGCCATTGTGGAGGATGATGGGCTCAGTGCAGCTTCACTGCTGTGCTCA  
 TGAACCTGGGTGATGTTTCAACATGCTCCATGACAACCTCAAGCCATGATCAGTTGAAATGGGCTTTTGAAGC  
 CTCTGCCATGTCATGGCCCTGTGATGGCTCATGTGGATCCTGAGGAGCCCTGGTCCCCCTGCAGTGGCCGCTT  
 CATCACTGACTCTCTGACAACTGGCTATGGCAGTCTCTCTAGACAACACAGAGCTCATTTGCTATGCTGTG  
 GATTTCCCTGGCAGAGCAATGATGTGCTAGCCAGTGGCCAGCTGACCTTCCGGGCCGATTCAGCCCATTTGCC  
 ACAGCTGGCCGCGCCCTGTGCTGCCCTCTGGTGTCTCGGCCACTCAATGGCATGCCATGCTATGTGCCACAATCA  
 CTCGCCCTGGCGCCATGGCACACCTCGCGGCCCGCACAGGCTGCATGGTGGTGTGCTGCTCCACATGGACCA  
 GCTCCAGGACTTCAATATCCACAGGCTGGTGGCTGGGGTCTTGGGAGCACTGGGTGATGCTCTCGACCTGT  
 TGGGGGTGGTCCAGTTCCTCCCGAGACTGCACGAGGCTGTCCCCCGAATGGTGGCAAGTACTGTGAGGG  
 CCGCCGTACCGGCTTCGCTCTGCAACACTGAGGACTGCCAACTGGCTCAGCCCTGACCTTCCGCGAGGAGCA  
 GTGTGCTGCCACAAACCCAGCAGCCGACCTCTTCAAGAGCTTCCAGGGCCCATGGATGGGTGCTCTCGCTACAC  
 AGCGGTGGCCCCCAGGACAGTGCAAACTCACTGCCAGGCCCGGGCAGCTGGGCTACTACTATGTGCTGGAGCC  
 ACGGTGGTAGATGGGACCCCTGTTCCCGGACAGCTCCTCGGTCTGTGTCCAGGGCGATGCATCCATGCTGG  
 CTGTGATCGCATTTGGCTCCAAGAAGAAGTTTGACAAGTGATGGTGTGCGAGGGGACGGTTCTGGTGTGAG  
 CAGTCAGTCAGGCTCCTTCAGGAAATTCAGGTACGGATAACAATGTGGTCACTATCCCCGGGGGGCCACCA  
 CATTTCTTGTCCGGCAGCAGGGAACCTCGGCCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGTGGCTCCTA  
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGGCAGCTGACTTGGCCTA  
 CAGCGGGCCACTGCAGCTCAGAGACACTGTCAAGCATGGGCCACTGGCCCACTGGCCACTTGAACCTGCAAGTCT  
 AGTGGCTGGCAACCCAGGACACAGCCTCCGATACAGTCTCTCGTGGCCCGGCCAGCCCTTCAAGCCCAAG  
 CCCCCTCCCCAGGACTGGCTGCACCGAAGAGCAGATTTCTGGAGTCTCTCGCGCGCCCTTGGCGGGCAG  
 GAA**TTAA**CTCACTATCCGGCTGCCCTTTCTGGGCACCGGGGCTCGGACTAGCTGGGAGAAAGAGAGGCT  
 CTGTTGCTGCCCTCATGCTAAGACTCAGTGGGGAGGGGCTGTGGGCTGAGACCTGCCCTCTCTCTGCCCTAAT  
 GCGCAGGCTGGCCCTCGCTCTGCTTCTCGCCCTGGGAGGCACTGATGGGTAGTGATGGAAGGGGCTGACAG  
 AGCCCTCCATCTAAACTGCCCTCTCGCTCGGGTCAAGAGGAGGGGGGAAGCAGGAGGGGCTGGGCC  
 CAGTTGATTTATTTAGTATTTATTA**CT**TTATTTAGCACAGGAAGGGGACAGGACTAGGCTCTGGGGAA  
 CTTGACCCCTGACCCCTCATGCGCTCACCTCGGGCTAGGAAATCCAGGCTGGTGGTATAGGTATGATGGTGGT  
 TGTGATTCGGTGTGGTGTGTGTGGAAATGTGTGTGTGCTATGATAGGATACAACCTGTTCTGCTTCTCTC  
 TTCTCGAATTTATTTTGGGAAAGAAAGTCAAGGGTAGGGTGGGCTTCAGGAGTGAAGGATATCTTTT  
 TTTT**TTTT**TTTTTTTTTTTTTTTTTTTTTGGAGACGAATCTCGCTCTGCGCCAGGCTGGAGTGCATG  
 GCACAACTCTCGGCTCATGCTACTCTCGGCTCCCGGGTCAAGTGATTTCACTCATGCTCAGCCTCTGATGAGTGC  
 GATACAGGCTCTCGCCACCGCCAGCTAATTTTTGTTTGTGTTTGGAGACAGAGTCTGCTATGTTGTC  
 CCGAGGCTGGATGATTTCAGCTCACTGCAACCTTCCGCCCTGGGTTCCAGCAATTTCTCGCTCAGGCTCC  
 CAGTACTGACGATTATAGCACTTACCACACCGCCGGCTAATTTTTGATTTTAGTAGACAGGGTTTACCAT  
 CATGTTGGCCAGGCTGGTCTCGAATCTGACCTTAGTGATCACTCGCCTCATCTCCCAAGTGGCTGGGAT  
 TACGGCGTGAGCCACCGTGGCTGGCCACGCCAACTAATTTTTGATTTTTAGTAGACAGGGTTTCACTATGT  
 TCGCCAGCTGCTCTTGAACCTGCTGACCTCAGGTAATCGACCTGCTCGGCCCTCCAAAGTGTGGGATTCAGG  
 TGTGAGCCACACGCGCGTACATATTTTTAAATGAATTTACTATTATGTGATCTTTTGGAGTCAGACAG

**FIGURE 179B**

ATGTGGTTGCATCCTAACTCCATGTCTCTGAGCATTAGATTCTCATTGGCCAATAATAATACCTCCCTTAGAAG  
TTTGTGTGAGGATTAAATAATGTAATAAAGAACTAGCATAACACTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
AAAGGAAA

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**FIGURE 180**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492

><subunit 1 of 1, 837 aa, 1 stop

><MW: 90167, pI: 8.39, NX(S/T): 1

MSQTGSHPRGLAGRWLWGAQPCLLLPVPLSWLVWLLLLLLASLLPSARLASPLPREEEIV  
FPEKLNGLSVLPQSGAPARLLCRLQAFGETLLLEQDSGVQVEGLTVQYLGQAPELLGGAEP  
GTYLTGTINGDPESVASLHWDGGALLGLVLYRGAELHLQPLEGGTPNSAGGPGAHILRRKSP  
ASGQGPMCNVKAPLGSPSPRRRAKRFRASLSRFVETLVVADDKMAAFHAGLKRYYLLTVMAA  
AAKAFKHPSIRNPVSLVTVRLVILGSGEEGPQVGPSAAQTLRSFCAWQRLNTPEDSGPDHF  
DTAILFTRQDLCGVSTCDTLGMADVGTVCDFARSCAIVEDDGLQSAFTAAHELGHVFNMLHD  
NSKPCISLNGPLSTSRHVMAVMAHVDPPEEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL  
PVTFFPKDYDADRQCQLTFGPDSRHCPQLPPPCAALWCSGHLNMGAMCQTKHSPWADGTPCG  
PAQACMGGRLHMDQLQDFNIPOAGGWGPWGPWGDCSRTCGGGVQFSSRDCTRPVPRNGGKY  
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLKFSFPGPMDWVPRYTGVAPODQCK  
LTCQARALGYYYVLEPRVVDGTPCSPDSSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG  
SGCSKQSGSFRKFRYGYNVVTIPAGATHILVRQQGNPGHRSIYLAKLPDGSYALNGEYTL  
MPSPTDVVLPGAVALRYSYGATAASETLSGHGFLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT  
PSTPRPTPDWLHRRRAQILEILRRRPWAGRK

**Important features of the protein:**

**Signal peptide:**

amino acids 1-48

**N-glycosylation site.**

amino acids 68-71

**Glycosaminoglycan attachment site**

amino acids 188-191, 772-775

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 182-185

**Tyrosine kinase phosphorylation site.**

amino acids 730-736

**N-myristoylation sites.**

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-  
172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-  
582, 679-684, 682-687, 763-768

**Amidation sites.**

amino acids 560-563, 834-837

**Leucine zipper pattern.**

amino acids 17-38, 24-45

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 358-367

**FIGURE 181**

CAGCAGTGGTCTCTCAGTCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**  
 CAAAGAATCCTCCAGAGAATTGTGAAGACTGTACATTCTAAATGCAGAAGCTTTTAAATCC  
 AAGAAAATATGTAAATCACTTAAGATTTGTGGACTGGTGTGTTGGTATCCTGGCCCTAACTCT  
 AATTGTCCTGTTTTGGGGGAGCAAGCACTTCTGGCCGGAGGTACCCAAAAAGCCTATGACA  
 TGGAGCACACTTTCTACAGCAATGGAGAGAAGAAGAAGATTTACATGGAATTGATCCTGTG  
 ACCAGAACTGAAATATTAGAAGCGGAAATGGCACTGATGAAACATTGGAAGTGCACGACTT  
 TAAAACGGATACACTGGCATCTACTTCGTGGGTCTTCAAAAATGTTTTATCAAAACTCAGA  
 TTAAAGTGATTCTGAAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC  
 ACAACTTTCTTTGAACAGTCAGTGATTTGGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA  
 TTTTCTTAAAAATTCAAAATTTCTGGAGATTTGTGATAACGTGACCATGTATTGGATCAATC  
 CCACTCTAATATCAGTTTCTGAGTTACAAGACTTTGAGGAGGAGGGAGAAGATCTTCACTTT  
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGGTGGTCCCTCAAGTGAAAGT  
 AGAGAAGACCCGTCACGCCAGACAAGCAAGTGAGGAAGAAGTTCCAATAAATGACTATACTG  
 AAAATGGAATAGAAATTTGATCCCATGCTGGATGAGAGAGGTTATTGTTGTATTTACTGCCGT  
 CGAGGCAACCGCTATTGCCGCCGCGTCTGTGAACCTTTACTAGGCTACTACCCATATCCATA  
 CTGCTACCAAGGAGGACGAGTCATCTGTCGTGTCATCATGCCTTGTAAGTGGTGGGTGGCCC  
 GCATGCTGGGAGGGTCT**TAA**TAGGAGGTTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT  
 AATAAATGCATGCTATTCAATGAATTTCTGCCTATGAGGCATCTGGCCCTGGTAGCCAGCT  
 CTCCAGAATTACTTGTAGGTAATTCCTCTCTTCATGTTCTAATAAACTTCTACATTATCACC  
 AAAAAAAAAAAAAAAAAA



**FIGURE 182**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFKSKICKSLKICGLVFGILALTILIVLFWGSKHFWPEVPPKAY
DMEHTFYSSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLVHDFKNGYTGIFYVGLQKCFIKT
QIKVIPEFSEPEEEIDENEEITTTFFEQSVIWPVPAEKPIENRDFLKNKILEICDNVTMYWI
NPTLISVSELQDFEEEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGEIEFDPMLDERGYCCIIYCRNRNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-40

**Transmembrane domain:**

amino acids 25-47 (type II)

**N-glycosylation sites.**

amino acids 94-97, 180-183

**Glycosaminoglycan attachment sites.**

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

**N-myristoylation sites.**

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

**Microbodies C-terminal targeting signal.**

amino acids 315-317

**Cytochrome c family heme-binding site signature.**

amino acids 9-14

**FIGURE 183**

GCGGAACTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCCGAGGGCCAGGGAGCTGCC  
 CGGCTGGCCTAGGCAGGCAGCCGCACCA**ATG**GCCAGCACGGCCGTGCAGCTTCTGGGCTTCCT  
 GCTCAGCTTCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACCTGGCGGAGGA  
 CAGCGCACGTGGGCACCAACATCCTCACGGCCGTGTCCTACCTGAAAGGGCTCTGGATGGAG  
 TGTGTGTGGCACAGCACAGGCATCTACCAGTGCCAGATCTACCGATCCCTGCTGGCGCTGCC  
 CCAAGACCTCCAGGCTGCCCCGCGCCCTCATGGTCATCTCCTGCCCTGCTCTCGGGCATAGCCT  
 GCGCCTGCGCCGTATCGGGATGAAGTGACGCGCTGCGCCAAGGGCACACCCGCCAAGACC  
 ACCTTTGCCATCCTCGCGGGCACCCCTCTTCATCCTGGCCGGCCTCCTGTGCATGGTGGCCGT  
 CTCTTGGACCACCAACGACGTGGTGCAGAACTTCTACAACCCGCTGCTGCCAGCGGCATGA  
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCTCGCTCATTGGT  
 GGCACCTGCTTTGCCTGTCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGGCC  
 CAGGGCCACCACGA<sub>4</sub>CACTGCAAACACCGCACCTGCCTACCAGCCACCAGCTGCCTACAAAG  
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGGTACAGGCTGAACGACTACGTG  
**TGAGT**CCCCACAGCCTGCTTCTCCCCTGGGCTGCTGTGGGCTGGGTCCCCGGCGGGACTGTC  
 AATGGAGGCAGGGTTCCAGCACAAAGTTACTTCTGGGCAATTTTGTATCCAAGGAAATA  
 ATGTGAATGCGAGGAAATGTCTTTAGAGCACAGGGACAGAGGGGGAAATAAGAGGAGGAGAA  
 AGCTCTCTATACCAAGACTGAAAAAAAAAATCCTGTCTGTTTTTGTATTATTATATATAT  
 TTATGTGGGTGATTTGATAACAAGTTAATATAAAGTGACTTGGGAGTTTGGTCAGTGGGGT  
 TGGTTTGTGATCCAGGAATAAACCTTGCGGATGTGGCTGTTTATGAAAAAAAAAAAA

**FIGURE 184**

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY  
 QCQIYRSLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAGTPAKTTFAILGGTL  
 FILAGLLCMVAVSWTTNDVVQNFYNPLLPSCMKFEIGQALYLGFISSSLIGGTLCLSCQ  
 DEAPYRPYQAPPRATTTTANTAPAYQPPAAYKDNRAFSVTSATHSGYRLNDYV

**Important features of the protein:****Signal peptide:**

amino acids 1-21

**Transmembrane domains:**

amino acids 82-103, 115-141, 160-182

**FIGURE 185**

GAGCTCCCCTCAGGAGCGGTTAGCTTCACACCTTCGGCAGCAGGAGGGCGGCAGCTTCTCG  
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATGT**CCACCACCACATGCCAAGTGGTGGCGTTCCT  
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCGGGATGGACATGTGGAGACCCC  
 AGGACCTGTACGACAACCCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC  
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCCTATTTACCATCCTGGGACTTCCAGC  
 CATGCTGCAGGCAGTGCAGGCCCTGATGATCGTAGGCATCGTCTGGGTGCCATTGGCCCTCC  
 TGGTATCCATCTTTGCCCTGAAATGCATCCGCATTGGCAGCATGGAGGACTCTGCCAAAGCC  
 AACATGACACTGACCTCCGGGATCATGTTTCATTGTCTCAGGTCTTTGTGCAATTGTCTGGAGT  
 GTCTGTGTTTGCCAACATGCTGGTGACTAACTTCTGGATGTCACAGCTAACATGTACACCG  
 GCATGGGTGGGATGGTGCAGACTGTTCCAGACCAGGTACACATTTGGTGGCGCTCTGTTCTGTG  
 GGCTGGGTGCCTGGAGGCCCTCACACTAATTGGGGGTGTGATGATGTGCATCGCCTGCCGGGG  
 CCTGGCACCAGAAGAAACCACTACAAGCCGTTTCTTATCATGCCTCAGGCCACAGTGTG  
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCACTGGCTTTGGGTCCAACACCAAAACAGAAG  
 ATATACGATGGAGGTGCCCGCACAGAGGACGAGGTACAATCTTATCCTTCCAAGCACGACTA  
 TGTGT**TAA**TGCTCTAAGACCTCTCAGCACGGGCGGAAGAACTCCCGGAGAGCTCACCCAAA  
 AACAAGGAGATCCCATCTAGATTTCTTCTTGCTTTTGACTCACAGCTGGAAGTTAGAAAAGC  
 CTCGATTTTCATCTTTGGAGAGGCCAAATGGTCTTAGCCTCAGTCTCTGTCTCTAAATATTC  
 ACCATAAAACAGCTGAGTTATTTATGAATTAGAGGCTATAGCTCACATTTTCAATCCTCTAT  
 TTCTTTTTTTAAATATAACTTTCTACTCTGATGAGAGAATGTGGTTTTAATCTCTCTCAC  
 ATTTTGATGATTTAGACAGACTCCCCCTCTTCTCCTAGTCAATAAACCCATTGATGATCTA  
 TTTCCAGCTTATCCCCAAGAAAACTTTTGAAAGGAAGAGTAGACCCAAAGATGTTATTTT  
 CTGCTGTTTGAATTTTGCTCCCCACCCCAACTTGGCTAGTAATAAACACTTACTGAAGAA  
 GAAGCAATAAGAGAAAGATATTTGTAATCTCTCCAGCCCATGATCTCGGTTTTCTTACACTG  
 TGATCTTAAAGTTACCAAAACAAAGTCATTTTCAGTTTGAGGCAACCAACCTTTCTACTG  
 CTGTTGACATCTTCTATTACAGCAACACCATTTCTAGGAGTTTCTGAGCTCTCCACTGGAG  
 TCCTCTTTCTGTGCGGGGTGAGAAATGTCCCTAGATGAATGAGAAAATTATTTTTTTAAAT  
 TTAAGTCCTAAATATAGTTAAATAAATAATGTTTTAGTAAATGATACACTATCTCTGTGA  
 AATAGCCTCACCCCTACATGTGGATAGAGGAATGAAAAATAATTGCTTTGACATTGTCT  
 ATATGCTACTTTGTAAAGTCATGCTTAAGTACAAATTCATGAAAGCTCACACCTGTAATC  
 CTAGCACTTTGGGAGGCTGAGGAGGAAGGATCACTTGAGCCAGAAGTTCCGAGACTAGCCTG  
 GGCAACATGGAGAAGCCCTGTCTCTACAAAATACAGAGAGAAAAAATCAGCCAGTCATGGTG  
 GCATACACCTGTAGTCCAGCATTCGGGAGGCTGAGGTGGGAGGATCACTTGAGCCAGGG  
 AGGTTGGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA  
 TCCTGTCTAAAAAATAAAAAATAAATAATGGAACACAGCAAGTCTAGGAAGTAGGTTAAA  
 ACTAATCTTTAA

**FIGURE 186**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSVFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIACRGLAPEETNYKAVSYHASGHSVAYKPGGFKASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

**Signal peptide:**

amino acids 1-23

**Transmembrane domains:**

amino acids 81-100, 121-141, 173-194

**FIGURE 187**

GGAAAACTGTTCTCTTCTGTGGCACAGAGAACCCTGCTTCAAAGCAGAAGTAGCAGTTCCG  
 GAGTCCAGCTGGCTAAAACTCATCCCAGAGGATAATGCAACCCATGCCTTAGAAATCGCTG  
 GGCTGTTTCTGGTGGTGTGGAATGGTGGGCACAGTGGCTGTCAGTGCCTCAGTGG  
 AGAGTGTGCGCCCTTCATTGAAAACAACATCGTGGTTTTTGAAAACCTCTGGGAAGGACTGTG  
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCTGCTGG  
 CTCTTTCTCCGACCTACAGGCAGCCAGAGGACTGATGTGTGCTGCTTCCGTGATGTCCTTC  
 TTGGCTTTTCATGATGGCCATCCTTGGCATGAAATGCACCCAGGTGCACGGGGGACAATGAGAA  
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTTCATCATCACGGGCATGGTGGTGC  
 TCATCCCTGTGAGCTGGGTGGCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT  
 GTTGCCCAAAAACGTGAGCTTGGAGAAGCTCTCTACTTTAGGATGGACCACGGCACTGGTGC  
 GATTGTTGGAGGAGCTCTGTTCTGCTGCGTTTTTGTGTGCAACGAAAAGAGCAGTAGCTACA  
 GATACTCGATACCTTCCCATCGCACACCCAAAAAGTTATCACACCGGAAAGAAGTCACCG  
 AGCGTCTACTCCAGAAGTCAGTATGTGTAGTTGTTGTTGTTTAACTTTACTATAAAGC  
 CATGCAAAATGACAAAAATCTATATTACTTTCTCAAATGGACCCCAAAGAACTTTGATTTA  
 CTGTTCTTAACTGCCTAATCTTAATTACAGGAACGTGTCATCAGCTATTATGATCTATAA  
 GCTATTTTCAGCAGAATGAGATATTAAACCCAATGCTTGTGATTGTTCTAGAAAGTATAGTAAT  
 TTGTTTTCTAAGGTGGTTCAAGCATCTACTCTTTTTATCATTACTTTCAAATGACATTGCT  
 AAAGACTGCATTATTTTACTACTGTAATTTCTCCACGACATAGCATTATGTACATAGATGAG  
 TGTAACATTTATATCTCACATAGAGACATGCTTATATGGTTTTATTTAAATGAAATGCCAG  
 TCCATTACACTGAATAAATAGAAGTCAACTATTGCTTTTCAGGGAAATCATGGATAGGGTTG  
 AAGAAGGTTACTATTAATGTTTAAAAACAGCTTAGGGATTAATGTCCTCCATTATATGA  
 AGATTTAAATGAAGGCTTTAATCAGCATTGTAAAGGAAATTGAATGGCTTCTGATATGCTG  
 TTTTTTAGCCTAGGAGTTAGAAATCCCTAACTTCTTTATCCTTCTCTCCAGAGGCTTTTTTT  
 TTCTTGTGTATTAAATTAACATTTTTTAAACGCAGATATTTTGTCAAGGGGCTTTGCATTCA  
 AACTGCTTTTCCAGGGCTATACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAAGTGATG  
 GTTTTAGGAAAGTGAAAAATTTTTGTTTTGTATTGGAAGAAGATGATGCATTTTGACAA  
 GAAATCATATATGATGGATATATTTTAATAAGTATTTGAGTACAGACTTTGAGGTTTCATC  
 AATAATAAATAAAGAGCAGAAAAATATGTCTTGGTTTTTCATTGCTTACCAAAAAACAACA  
 ACAAAAAAGTTGTCTTTGAGAACCTCACCTGCTCTATGTGGGTACCTGAGTCAAAATG  
 TCATTTTTGTTCTGTGAAAAATAAATTTCTTCTTGTACCAATTTCTGTTTAGTTTTACTAAA  
 ATCTGTAATACTGTATTTTTCTGTTTATTCCAAATTTGATGAAACTGACAATCCAATTTGA  
 AAGTTTGTGTCGAGCTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTTATACATTTATA  
 TTAATAAATGTACATTTTCTAATT

**FIGURE 188**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLALSPDLQAARGLMCAASVMSFLAFMMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWVANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

**Signal peptide:**

amino acids 1-17

**Transmembrane domains:**

amino acids 82-101, 118-145, 164-188

**FIGURE 189**

TCGCC**ATG**GCCTCTGCCGGAATGCAGATCCTGGGAGTCGTCCTGACACTGCTGGGCTGGGTG  
AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAGGTGACCGCTTTCATCGGCAACAGCAT  
CGTGGTGGCCAGGTGGTGTGGGAGGGCCTGTGGATGTCTCGCTGGTGCAGAGCACCGGCC  
AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGCTGCCACAGGACCTGCAGGCTGCACGT  
GCCCTCTGTGTATCGCCCTCCTTGTGGCCCTGTTGGCTTGTCTGCTACCTTGTCTGGGGC  
CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCCTGGTGCTCACCTCTGGGA  
TTGTCTTTGTATCTCAGGGGTCTGACGCTAATCCCCGTGTGCTGGACGGCGCATGCCATC  
ATCCGGGACTTCTATAACCCCTGTGTGGCTGAGGCCCAAAGCGGGAGCTGGGGGCCCTCCCT  
CTACTTGGGCTGGGCGGCCCTCAGGCCTTTTGTGTGCTGGGTGGGGGGTTGTCTGTCTGCATT  
GCCCCCTCGGGGGGGTCCCAGGGCCCCAGCCATTACATGGCCCCGCTACTCAACATCTGCCCT  
GCCATCTCTCGGGGGGCCCTCTGAGTACCCTACCAAGAATTACGTCT**TGA**CGTGGAGGGGAATG  
GGGGCTCCGCTGGCGCTAGAGCCATCCAGAAGTGGCAGTGCCCAACAGCTTTGGGATGGGTT  
CGTACCTTTTGTCTTCTGCCTCCTGCTATTTTCTTTTGACTGAGGATATTTAAAATTCATTT  
GAAACTGAGCCAAGGTGTGACTCAGACTCTCACTTAGGCTCTGCTGTTTCTCACCTTGG  
ATGATGGAGCCAAGAGGGGATGCTTTGAGATTCTGGATCTTGACATGCCCATCTTAGAAGC  
CAGTCAAGCTATGGAACATAATGCGGAGGCTGCTTGTGTGCTGGCTTTGCAACAAGACAGAC  
TGTCCCCAAGAGTTCCTGCTGCTGCTGGGGCTGGGCTTCCTTAGATGTCACTGGACAGCTG  
CCCCCATCCTACTCAGTCTCTGGAGCTCCTCTCTTCACCCCTGGAAAAACAAATCATCTG  
TTAACAAAGGACTGCCACCTCCGGAACCTCTGACCTCTGTTTCTCCGTCTGATAAGACG  
TCCACCCCCAGGGCCAGGTCCAGCTATGTAGACCCCCGCCCCACCTCCAACACTGCACC  
CTTCTGCCCTGCCCCCTCGTCTCACCCCTTACACTCACATTTTTATCAAATAAAGCATG  
TTTTGTTAGTGCA



**FIGURE 190**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNLVSCALPMWKVTAFIGNSIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSSLALPQDLQAARALCVIALLLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSGIV
FVISGVLTLPVCWTAHAIIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCCTCP
SGGSQGQPSHYMARYSTSAPAIISRGPSSEYPTKNYV
```

**Transmembrane domains:**

amino acids 8-30 (type II), 82-102, 121-140, 166-186

193/249

**FIGURE 191**

GCCAAGGAGAACATCATCAAGACTTCTCTAGACTCAAAGGCTTCCACGTTCTACATCTTG  
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTTCAAAGTAAAGGCAATGGCATTTTATCCC  
 TTGCAAATTGCTGGGCTGGTTCTTGGGTTCCTTGGCATGGTGGGACTCTTGCCACAACCCT  
 TCTGCCTCAGTGGTGGAGTATCAGCTTTTGTGGCAGCAACATTATTGTCTTTGAGAGGCTC  
 TGGGAAGGGCTCTGGATGAATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA  
 TAGCTCCTTGTGTGGCTCTCCCGCTGCCCTGGAACAGCCCCGGGCCCTCATGTGTGTGGCTG  
 TTGCTCTCTCCTTGATCGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA  
 GGCTCTAACGAGAGGGCCAAAGCATACCTTCTGGGAACCTCAGGAGTCCCTCTTCATCCTGAC  
 GGGTATCTTCGTTCTGATTCGGGTGAGCTGGACAGCCAATATAATCATCAGAGATTTCTACA  
 ACCCAGCCATCCACATAGGTGAGAAACGAGAGCTGGGAGCAGCACTTTTCCTTGGCTGGGCA  
 AGCGCTGCTGTCCTCTTCATTGGAGGGGGTCTGCTTTGTGGATTTTGTGCTGCAACAGAAA  
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACAGATAAGCGAAGAA  
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTCTTAATGCCTCCCTTTTGGCTCCAAGT  
 ATGGACTATGGTCAATGTTTTTTATAAAGTCCTGCTAGAACTGTAAGTATGTGAGGCAGGA  
 GAACTTGCTTTATGTCTAGATTACATTGATACGAAAGTTTCAATTTGTTACTGGTGGTAGG  
 AATGAAAATGACTTACTTGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG  
 GACCCAATCGCTGCTCCAATTTTCATATTCTAAATTCAAGTATACCATAATCATTAGCAAG  
 TGTACAATGATGGACTACTTATTACTTTTTGACCATCATGTATTATCTGATAAGAATCTAAA  
 GTTGAAATTGATATTCTATAACAATAAACATATACCTATTCTA

**FIGURE 192**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPVSWTANIIIRD FYNPAIHIGQKRELGAALFLGWASAAVL
FIGGGLLCGFCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLS KTSTSYV
```

**Important features of the protein:****Transmembrane domains:**

amino acids 31-51, 71-90, 112-133

**N-glycosylation site.**

amino acids 161-164

**FIGURE 193**

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTTCCAGC**CATG**AAGATCACTGGGGGT  
CTCCTTCTGCTCTGTACAGTGGTCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC  
AAAAAAGTGGACTGCAGCATTTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCCATCA  
CATACCTACCAGTTTGTGGTCTGACTACATCACCATATGGGAATGAATGTCACTTGTGTACC  
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTTCTTCACGATGGAAGTTGC**TAA**ATTCTCCA  
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCATCATCCCAGGCTCTGACTG  
AGTTTCTTTCAGTTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTAGAGTAATCTTG  
ACTGAATGGAGAAAGTTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT  
TTTTTTTTTAACACGTCAATAAAAAAATAATCTCCAGA



**FIGURE 195**

CCCGCGCCCGGTTCTCCCTCGCAGCACCTCGAAGTGC GCCCTCGCCCTCCTGCTCGCGCCC  
CGCCGCC**ATG**GCTGCCTCCCCGCGCGGCCTGCTGTCTTGGCCCTGACCGGGCTGGCGCTGC  
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTTCAA  
AAACGAGAAGCACCTGTTCCAATAAGACTAAAGTGGCCGTTGATGAGAATAAAGCCAAAGA  
ATTCTTGGCAGCCTGAAGCGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCCGAGGTGC  
AGCAGTGGTACCAGCAGTTTCTCTACATGGGCTTTGATGAAGCGAAATTTGAAGATGACATC  
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA  
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCCCTACGGCTTTAGGCATGGAGCCAGCG  
TCAACTACGATGACTACT**TA**ACCATGACTTGCCACACGCTGTACAAGAAGCAAATAGCGATTCT  
CTTTCATGTATCTCCTAATGCCTTACACTACTTGGTTTCTGATTTTGCTCTATTTTCAGCAGAT  
CTTTTCTACCTACTTTGTGTGATCAAAAAAGAAGAGTTAAACAACACATGTAAATGCCTTT  
TGATATTTTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAAGCATTTTGTAAAAAGA

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></usr/seqdb2/ssc/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTLGLALLLLCWGGPGGISGNKLKLMQLKREAPVPTKTKVAVDENKAKEFL
GSLKRQKRQLWDRTRFEVQQWYQQFLYMGFDEAKFEDDITYWLNLRDRNGHEYGYDYYQRHYD
EDSAIGPRSPSYGFRHGASVNVYDDY
```

Signal peptide:

amino acids 1-30

**FIGURE 197**

CGGCTCGAGCCCGCCCGGAAGTGCCCGAGGGGCGCGATGGAGCTGGGGGAGCCGGGCGCTC  
GGTAGCGCGGCGGGCAAGGCAGGCGCC**ATG**ACCTGATTGAAGGGGTGGGTGATGAGGTGAC  
CGTCTTTTCTCGGTGCTTGCTGCCTTCTGGTGCTGGCCCTTGCTGGGTCTCAACGCACA  
CCGCTGAGGGCGGGACCACTGCCCCAGCCGTCAGGGACCCCAACGCCATCCCAGCCAGC  
GCAGCCATGGCAGCTACCGACAGCATGAGAGGGGAGGCCAGGGGCAGAGACCCAGCCT  
GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCAGACGGGGTTACAGCAACACCGCCAG  
CCCCGGACTCCCCGACAGGAGCCCTCGTGCTACGGCTGAAATTCCTCAATGATTACAGAGCAG  
GTGGCCAGGGCCTGGCCCCACGACACCATTGGCTCCTTGAAAAGACCCAGTTTCCCGGCCG  
GGAACAGCAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCTGG  
GCAGCCTTACCTCCCTCCCAACTGCGTTCTCCACTGCCACGTGTCCACGAGAGTCGGTCCC  
CCAAATCCCCCTGCCCGCGGGGTCCGAGCCCGGCCCTCCGGGCTGGAAATCGGCAGCCT  
GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGGC  
CCTTCTTTCCCTGACCGCCACTCTGGGCCTGGCCGGCTTACCCCTGCTCCTCAGCTTCCTG  
GCCTTTGCCATGTACCGCCCG**TAG**TGCCCTCCGCGGGCGCTTGCCAGCGTCGCCGGCCCTCC  
GGACCTTGCTCCCCGCGCGCGCGGGAGCTGCTGCCTGCCAGGCCCGCCTCTCCGGCCTG  
CCTCTTCCCGCTGCCCTGGAGCCAGCCCTGCGCCGAGAGGACTCCCGGGACTGGCGGAGG  
CCCCGCCCTGCGACCGCGGGGCTCGGGGCCACCTCCCGGGGCTGCTGAACCTCAGCCCGCA  
CTGGGAGTGGGCTCCTCGGGGTGGGCATCTGCTGTCGCTGCCTCGGCCCGGGCAGAGCCG  
GGCCGCCCGGGGGCCGTCTTAGTGTTCTGCCGGAGGACCCAGCCGCCTCAATCCCTGAC  
AGCTCCTTGGGCTGAGTTGGGACGCCAGGTCGGTGGGAGGTGGTGAAGGGGAGCGGGAG  
GGGCAGAGGAGTTCCCCGGAACCCGTGCAGATTAAAGTAACGTGTGAAGTTTAAAAAAAAA  
AAAAAAA



**FIGURE 198**

MTLIEGVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM  
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVLRKFLNDSEQVARAWPHDT  
IGSLKRTQFPGREQQVRLIYQGQLLGDDTQTLGSLHLPNCVLHCHVSTRVGPPNPCCPPGS  
EPGPSGLEIGSLLLPLLLLLLLLLLWYCQIQYRPFPLTATLGLAGFTLLLSLLAFAMYRP

**Signal peptide:**

amino acids 1-31

**Transmembrane domain:**

amino acids 195-217

**FIGURE 199**

GAGATTGAAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG  
 ATTCCCCAGGCTCTCAGAGAAGATCAGCAGAAAAGTCTGCAAGACCCTAAGAACCATCAGCCC  
 TCAGCTGCACCTCCTCCCCTCCAAGG**ATG**ACAAAAGGCGCTACTCATCTATTTGGTCAGCAGC  
 TTTCTTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT  
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTTGTGG  
 AAAGCAAGTTCAACATATCAAAGATAAATGAAATGCGGATGGAAGCTTTGACTATGGCCTC  
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAAACCTTTGCCA  
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAAGGCATCCACTGCGCAAAAAGGA  
 TTGTGTCCGGAGCACGGGGGATGAACAACCTGGGTAGAATGGAGGTTGCACTGTTCAAGGCCGG  
 CCACTCTCCTACTGGCTGACAGGATGCCGCCTGAGAT**TGA**AACAGGGTGCGGGTGACCGTGG  
 AGTCATTCCAAGACTCCTGTCTCTACTCAGGGATTCTTCATTTCTTCTTCTCTACTGCCTCCA  
 CTTCATGTTATTTTCTTCCCTTCCCATTTACAACATAAACTGACCAGAGCCCCAGGAATAAA  
 TGGTTTTCTTGGCTTCTCCTTACTCCCATCTGGACCCAGTCCCCTGGTTCCTGTCTGTTAT  
 TTGTAAACTGAGGACCACAATAAGAAATCTTTATATTTATCG

**FIGURE 200**

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHYWCNDYKSYSENLC HVDCQDLLNP NLLAGIHC AKRIVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
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**Signal peptide:**

amino acids 1-18

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**FIGURE 201**

TCTGACCTGACTGGAAGCGTCCAAGAGGGACGGCTGTACGCCCTGCTTGACTGAGAACCCA  
 CCAGCTCATCCCAGACACCTCATAGCAACCTATTATACAAAGGGGGGAAGAAACCTGAG  
 CAGAATGGAATCATTTATTTTTTCCCAAGGAGAAAACCGGGTAAGGGGAGGGAAGCAATTC  
 AATTTGAAGTCCCTGTGAATGGGCTTTTCAGAAGGCAATTAAGAATAATCCACTCAGAGAGGAC  
 TTGGGGTGAACCTTGGGTCTGTGGTTTTCTGATTGTAAGTGGAAGCAGGTCCTGCACACGC  
 TGTGGGCAAAATGTGAGGACCAAGGTTAAGTGACTGGCAGAAAACCTCCAGGTGGAACAAGCA  
 ACCCATGTTCTGCTGCAAGCTTGAAGGAGCCTGGAGCGGGAGAAAGCTAAGCTTGAACATGAC  
 CTGTTGCAATTTGGCAAGTTCTAGCAACATGCTCCTAAGGAAGCGATACAGGCACAGACCATG  
 CAGACTCCAGTTCTCTCTGCTGCTCCTGATGCTGGGATGCGTCCTGATGATGGTGGCGATGT  
 TGCACCTCCCCACCACACCTGACACGACTGTCACAGCCCAAGCCAGCAAGCACAGCCCT  
 GAAGCCAGGTACCGCTGGACTTTGGGGAATCCAGGATTGGGTACTGGAAGCTGAGGATGA  
 GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCTTTATCTCACTGCGGGAGGATCAGC  
 TGCTGGTGGCCGTGGCCCTTACCCAGGCCAGAAAGCAAGAGCCAGGGCAGGAGAGGTGGG  
 AGCTACCGCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAGAGGGAAGTGGGG  
 GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTTAGCCTGGACCCAC  
 GTGGCCTCCAGGAGGCCTCAGTGCCCGCATCCCCCTCCAGAGGGCTCTGCCCGAGGTGCGG  
 CACCCACTGTGTCTGACGACGACCCCTCAGGACAGCCTGCCCCAGGCCAGCGTCATCTCTGT  
 TTTCCATGATGAGGCCTGGTCCACTCTCTGCGGACTGTACACAGCATCTCGACACAGTGC  
 CCAGGGCCTTCTGAAGGAGATCATCTCTGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG  
 TCTGCTCTCAGCAATATGTGGCCAGGCTGGAGGGGTGAAGTTACTCAGGAGCAACAAGAG  
 GCTGGGTGCCATCAGGGCCCGGATGCTGGGGGCCACAGAGCCACCGGGGATGTGCTCGTCT  
 TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCTCTCAGCAGAATAGCT  
 GGTGACAGGAGCCGAGTGGTATCTCCGGTGATAGATGTGATTGACTGGAAGACTTTCCAGTA  
 TTACCCCTCAAAGGACCTGCAGCGTGGGGTGTGGACTGGAAGCTGGATTTCACCTGGGAAC  
 CTTTGGCAGAGCATGTGAGGAAGGCCCTCCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG  
 GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCCAAAACACTGGAGCGTATGACTC  
 TCTTATGTGCTGCGAGGTGGTGAACCTCGAACTGTCTTTCAAGGCCCTGGCTCTGTGGTG  
 GCTCTGTTGAAATCCTTCCCTGCTCTCGGGTAGGACACATCTACCAAAATCAGGATTCCTAT  
 TCCCCCTCGACAGGAGGCCACCTGAGGAACAGGGTTCGCATTGCTGAGACCTGGCTGGG  
 GTCATTCAAAGAAACCTTCTACAAGCATAGCCCAGAGGCCCTCTCCTTGAGCAAGGCTGAGA  
 AGCCAGACTGCATGGAACGCTTGCAGCTGCAAAAGGAGACTGGGTTGTGCGACATTCACATGG  
 TTTCTGGCTAATGTCTACCCTGAGCTGTACCCATCTGAACCCAGGCCAGTTTCTCTGGAAA  
 GCTCCACAACACTGGACTTGGGCTCTGTGCAGACTGCCAGGCAGAAAGGGACATCTGGGCT  
 TCCCATGTGTGGTCTCTTGCAGTGACAGCCGGCAGCAACAGTACCTGCAGCACACCAGC  
 AGGAAGGACATTCACTTTGGCAGGCCACAGACCTGTGCTTGTGCTGTGAGGAGGAGCAGGT  
 GATTCTTCAGAACTGCACGGAGGAAGGCCGTGGCCATCCACAGCAGCAGTGGGACTTCCAGG  
 AGAATGGGATGATTGTCCACATTTCTTCTGGGAAATGCATGGAAGCTGTGGTGAAGAAAAC  
 AATAAAGATTTGTACCTGCGCTGTGATGGAAGCCCGCCGACAGTGCCGATTTGACCA  
 GATAAATGCTGTGGATGAACGATGAATGTCAATGTGAGAAGGAAAAGAAATTTTGGCCATC  
 AAAATCCAGCTCCAGTGAACGTAAGAGCTTATATATTTCATGAAGCTGATCTTTGTGTG  
 GTGTGCTCCTTGTGTTAGGAGAGAAAAAGCTCTATGAAAGAATATAGGAAGTTTCTCCTTT  
 TCACACCTTATTTTCATGACTGCTGGCTGCTTA

**FIGURE 202**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760  
><subunit 1 of 1, 639 aa, 1 stop  
><MW: 73063, pI: 6.84, NX(S/T): 2  
MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQT VTAQASKHSPEARYRLDFG  
ESQDWVLEAEDEGEEYSPLEGLPPFISLREDQLLVAVALPQARRNQSQGRRGGSYRLIKQPR  
RQDKEAPKRWDGADEGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP  
QDSLPTASVILCFHDEAWSTLLRTVHSILDTVPRAFLKEIILVDDLSQQQQLKSALSEYVAR  
LEGVKLLRSNKR LGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVSP  
VIDVIDWKTFFQYYP SKDLQRGVLDWKLD FHWEP LPEHVRKALQSPISPIRSPVVPGEVVAMD  
RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSV EILPCSRVGH IYQNQDSHSP LDQEATL  
RNRVRIAETWLG SFKETFYKHSPEAFSLSKAEKPD CMERLQLQRR LGCRT FHWFLANVY PEL  
YPSEPRPSFSGK LHN TGLGLCADCQAE GDILGCPMVL APCSDSRQQQYLQHTSRKEIHFGSP  
QHLCFAVRQE QVILQNCTEEGLAIHQHWD FQENGMI VHI LSGKCM EAVVQEN NKDLYLRPC  
DGKARQQWRFDQINAVDER

**Signal peptide:**

amino acids 1-28

**FIGURE 203**

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA  
 GTCCAGGATGTGGCCTGCGCTGCTGCTGTCCACCTCCTCCTCTCTGGCCACTGCTGTTGC  
 TGCCCTCCCACGCGCTGCTCAGGGCTCTTCATCCTCCCTCGAAGCCCCACGAGCCCCAGCC  
 CGCCCCCGTGTGCCAGGGGAGGCCCCCTCGGCCCCAGCTCATGTGTGCGTGTGGGAGCGAGC  
 ACCCTCCACCAAGCCGATCTCCTCGGGTCCCAGATCACGTCCGCAAGTCTCTGCTTGGCACTG  
 CACCCCCAGCCACCCCATCAGGCTTTGAGGAGGGGCGCCCTCATCCCAATACCCCTGGGCT  
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGGACCCCAACTCTGCCAATCCCGG  
 ATTTCTGGACTATGGTTTTGCAGCCCCCTCATGGGCTCGCAACCCACACCCCAACTCAGACT  
 CCATGCGAGGTGATGGAGATGGGCTTATCCTTGGAGAGGCACCTGCCACCTTGGGCCATTCT  
 CTGTTCTGGGGGCGGTGGGGAAGGTGTGGACCCCAAGCTCTATGTACAAATTACCATCTCCAT  
 CATCATTTGTTCTCGTGGCCACTGGCATCATCTTCAAGTTCTGCTGGGACCCGAGCCAGAAGC  
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGAGCCAGCAGCCACTGACA  
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGGCTTGGGGACTCACCTACCCCAACCC  
 TGACCATGAGGAGCCCCGAGGGGACCCGCGCTGGGATGCCCCACCCCAAGGGGGCTCCAG  
 CCTTCCAGTTGAACCGTGAAGGGCAGGGGCAATGGGATGGGAGGGCAAGAGGGGAAGGCAAC  
 TTAGGTCTTCAGAGCTGGGGTGGGGTGCCCTCTGGATGGGTAGTGAGGAGGCAGGCGGTGC  
 CTCCACAGCCCTTGGCCCTCCCAAGGGGGCTGGACCAGCTCCTCTCTGGGAGGCACCCCTTC  
 CTTCTCCCAGTCTCTCAGGATCTGTGTCTTATTTCTGCTGCCCCATAACTCCAACCTCTGCC  
 TCTTTGGTTTTTTTCTCATGCCCACCTGTCTAAGACAACCTGCCCCCTTAACCTTGATTCCC  
 CCTCTTTGTCTTGAACCTTCCCCTTCTATTTCTGGCCTACCCCTTGGTTCCTGACTGTGCCCTT  
 TCCCCTTCTCCTCTCAGGATTCCTCTGGTGAATCTGTGATGCCCCCAATGTTGGGGTGCAGCC  
 AAGCAGGAGGCCAAGGGGCGGCACAGCCCCATCCCAGTGAGGCTGGGGCAGCTGTGGGGA  
 GCTGGGGCCACAGGGGCTCCTGGCTCCTGCCCTTGACACACCCGGAACACTCCCCAGCC  
 CCACGGGCAATCCTATCTGCTCGCCCTCCTGCAGGTGGGGCTCACATATCTGTGACTTCG  
 GGTCCCTGTCCCCACCTTGTGCACTCACATGAAAGCCTTGCACTACCTCCACCTTCAC  
 AGGCCATTTGCACACGCTCCTGCACCCCTTCCCCGTCCATACCGCTCCGCTCAGCTGACTCT  
 CATGTTCTCTCGTCTCACATTTGCACTCTCTCCTTCCCACATTTGTGCTCAGCTCACTCAG  
 TGGTCAGCGTTTCTGCAACATTTACCTCTCATGTGCGTTTCCCGGCTGATGTTGTGGTGG  
 TGTGCGGCGTGTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAAGCCCTGC  
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGGCTCCTTGGGCCCTCATCGGTATGG  
 TCTCGTCCCATTCACACCATTTGTTTCTCTGTCTCCCCATCCTACTCCAAGGATGCCGGCA  
 TCACCTGAGGGCTCCCCCTTGGGAATGGGGTAGTGAGGCCCCAGACTTACCCCCAGCCCCA  
 CTGCTAAATCTGTTTTCTGACAGATGGGTTTTTGGGAGTCGCTGCTGCACTACATGAGAA  
 AGGGATCTCCCATTTGCCCTTCCCTTTCTCCTACAGTCCCTTTTGTCTTGTCTGTCCTGGCTG  
 TCTGTGTGTGCTGCACTTCTCTGGACTTCAGAGCCCCCTGAGCCAGTCTCCCTTCCCAGCCT  
 CCTTTGGGGCTCCCTAACTCCACCTAGGCTGCCAGGGACCGGAGTCAGTGGTTCAAGGCC  
 ATCGGGAGCTCTGCTCCAAAGTCTACCCCTCCCTTCCCGGACTCCCTCTGTGCCCTTCTT  
 CCTCCCTCCTTCCACTCTCCTTCCCTTTTGTCTTCCCTGCCCTTCCCCCTCCTCAGGTT  
 CTTCCCTCCTTCTCACTGGTTTTCACCTTCTCCTTCCCTTCTTCCCTGGCTCCTAGGCT  
 GTGATATATTTTTGTATTATCTTTCTTCTTCTGTGGTGATCATCTTGAATTACTGTG  
 GGATGTAAGTTTCAAATTTTCAAATAAGGCTTTGCAAGATAA

**FIGURE 204**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPGAGV
PGRDGSPGANVIPGTPGIPGRDGFKEGEGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGGLPIEAIIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217

**FIGURE 205**

GTTAACCAGCGCAGTCCTCCGTGCGTCCCGCCCGCGCTGCCCTCACTCCCGGCCAGG**ATGG**  
CATCCTGTCTGGCCCTGCGCATGGCGCTGCTGCTGGTCTCCGGGGTTCTGGCCCTGCGGTG  
CTCACAGACGATGTTCCACAGGAGCCCGTGCCACGCTGTGGAACGAGCCGGCCGAGCTGCC  
GTCGGGAGAAGGCCCCGTGGAGAGCACAGCCCCGGCGGGAGCCCGTGGACACCGGTCCCC  
CAGCCCCCACCGTCGCGCCAGGACCCGAGGACAGCACCGCGCAGGAGCGGCTGGACCAAGGGC  
GGCGGCTCGCTGGGGCCGGCGCTATCGCGGCCATCGTGATCGCCGCCCTGCTGGCCACCTG  
CGTGGTGTGGCGCTCGTGGTCGTGCGCTGAGAAAGTTTTCTGCCTCCT**TGA**AGCGAATAAA  
GGGGCCGCGCCCGGCCGCGCGCGACTCGGCAAAAAAAAAAAAAA



**FIGURE 206**

>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398  
><subunit 1 of 1, 121 aa, 1 stop  
><MW: 12073, pI: 4.11, NX(S/T): 0  
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVVESTSPGREPVDTG  
PPAPTVPAGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 91-110

**Glycosaminoglycan attachment site.**

amino acids 44-47

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 116-119

**N-myristoylation site.**

amino acids 91-96

**FIGURE 207**

GGCCGTTGGTTGGTGCGCGGTGAAGGGTGTGGCGCAGCAGCGTCGTTGGTTGGCCGGCGG  
CGGGCCGGGACGGGC**ATGG**CCCTGCTGCTGTGCTTGGTGTGCTGACGGCGGCGCTGGCCCA  
CGGCTGTCTGCACCTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA  
ACTTCAAGTCCTGCTGGTGGGTGGGCGACATCCCCGTGTGAGGGCGCTGCTCACCAGCTGGAGC  
GACGACACGATGAAGGAGCTGCACCTGGCCATCCCCGCCAAGATCACCCGGGAGAAGCTGGA  
CCAAGTGGCGACAGCAGTGTACCAGATGATGGATCAGCTGTACCAGGGGAAGATGTACTTCC  
CCGGGTATTTCCCAACGAGCTGCGAAACATCTTCCGGGAGCAGGTGCACCTCATCCAGAAC  
GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGGAGGAGGGCAGCTCTCCAGGGAGGG  
ACCCAGCCTAGCACCTGAAGGATCAATGCCATCACCCCGGGGACCTCCCC**TAA**GTAGCCC  
CCAGAGGCGCTGGGAGTGTGCCACCGCCCTCCCTGAAGTTTGCTCCATCTCACGCTGGGG  
GTCAACCTGGGGACCCCTTCCCTCCGGGCCATGGACACACATACATGAAAACAGGCCGCAT  
CGACTGTGACACCGCTGTGGCATCTTCCAGTACGAGACCATCTCCTGCAACAACCTGCACAG  
ACTCGCAGCTCGCCTGCTTTGGCTATAACTGCGAGTAGGGCTCAGGCATCACACCACCCGT  
GCCAGGGCCCTACTGTCCTGGGGTCCAGGCTCTCCTTGGAGGGGCTCCCCGCCTTCCAC  
CTGGCTGTGTCGCGGTAGGGCGGGGCCGTGGGTTGAGGGGCGCACCACTTCCAAGCCTGTGT  
CCCACAGGTCTCGCGCAGTGAAGTCAGCTGTCCAGGGCCTCTGAACTACATAAATAAC  
TGGCACAAGTAAGTCCCCTCCTCAAACCAACACAGGCAGTGTGTGTATGTGAGCACCTCGTG  
GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCCAGCTCCTAGAGGGGCTCCCGA  
GGAGGTGGAACCTCAACCAGCTCTGCGCAGGAGCGGCTGCAGTCTTTTCTCCCTCAAAG  
GTCTCCGACCCTCAGCTGGAGGGCGGCATCTTCTTAAAGGGTCCCATAGGGTCTGGTTCC  
ACCCCATCCCAGGTCTGTGGTCAGAGCCTGGGAGGGTTCCCTACGATGGTTAGGGGTGCCCC  
ATGGAGGGGCTGACTGCCCCACATTCGCTTTTCCAGACAGGACACGAGCATGAGGTAAGGCCGC  
CCTGACCTGGACTTCAGGGGGAGGGGGTAAAGGGAGAGAGGAGGGGGGCTAGGGGGTCTCT  
AGATCAGTGGGGGCACTGCAGGTGGGGCTCTCCCTATACCTGGGACACCTGCTGGATGTCAC  
CTCTGCAACCACACCCATGTGGTGGTTTCATGAACAGACCAGCTCCTCTGCCTTCTCCTGG  
CCTGGGACACACAGAGCCACCCCGCCTTGTGAGTGACCCAGAGAAGGGAGGCCCTCGGGAGA  
AGGGGTGCTCGTAAGCCAACACAGCGTGCCGCGGCCTGCACACCCCTTCGGACATCCAGGC  
ACAGGGTGTGCTGGATGTGGCCACATAGGACCACACGTCCTCAGCTGGGAGGAGAGGCCT  
GGGGCCCCAGGGAGGGAGGCAGGGGGTGGGGGACATGGAGAGCTGAGGCAGCCTCGTCTCC  
CCGACAGCCTGGTATCGCGAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT  
TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGGCCTGCCCGAGGCAAC  
GTGGGGGCGGAGACTCAGCTGGACAGCCCTGCCTGTCACTCTGGAGCTGGGCTGCTGCTGC  
CTCAGGACCCCTCTCCGACCCCGACAGAGCTGAGCTGGCCAGGGCCAGGAGGGCGGGAGG  
GAGGGAATGGGGTGGGCTGTGCGCAGCATACGCGCTGGGCAGGTCCGACAGCTGCGGGA  
TGTGATTAAAGTCCCTGATGTTCTC

**FIGURE 208**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399

><subunit 1 of 1, 157 aa, 1 stop

><MW: 17681, pI: 7.65, NX(S/T): 1

MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK  
ELHLAIPAKITREKLDQVATAVYQMMQLYQGKMYFPGYFPNELRNIFREQVHLIQNAIIER  
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP

**Signal peptide:**

amino acids 1-15

**FIGURE 209**

AGCAGGAGCAGGAGAGGGGACAAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCTCTTATTTCT  
 CCTCACGTTGTAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCTCG  
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCAGCTGCCATGGAATTCATTGCTGCC  
 ACTGAGGTGGCTGTATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCACTACTCCA  
 TAGCATGGTGCAAAAATTCAGGCGTGTATTGGGATCAGCACATGATCTGAGGTTCTGA  
 CACACTACAACATCACTGGGAACACCATCTGCCTCTTTTCGCTGGTAGACAATGAACAACATG  
 AATTTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAAATTGAGCCGTTTCATTGAGAT  
 CAACAGCCTCCACATGGTGACAGAGTACAACCCGTGACTGTGATTGGGTTATTCAACAGCG  
 TAATTCAGATTCTCTCTCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG  
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATCTGGTGGACAG  
 TGGTATGAAGAAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAG  
 CTTTGGCAATTTACCAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTTCC  
 GTAGAGCATGTGCAAACTTTTGTGATGGATTCTTAAGTGAAAAATTGTTGAAAGAAAAATCG  
 TGAATCAGAAGGAAAGACTCCAAGGTGGAACCTTGACTTCTCCTTGGAACACATATGGCC  
 AAGTATCTACTTTATGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG  
 GATCACTAGGCCTGCCAACACACACACACGACGTCACACACGACGACGCGTGCACAC  
 ACACACGCGCACACACACACACACAGAGCTTCATTTCTGTCTTAAAAATCTCGTTTTCTC  
 TTCTTCTCTTTTAAATTCATATCCTCACTCCCTATCCAAATTCCTTCTTATCGTGCATT  
 CATACTCTGTAAGCCCATCTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATG  
 CCTCTATGAAAGAGAGGCATTCCCTAGAGAAAGATTGTTCCAATTTGTCAATTAATATCAAGT  
 TTGTATACTGCACATGACTTACACACAACATAGTTCTCTGCTCTTTTAAGGTTACCTAAGGGT  
 TGAAACTCTACCTTCTTTTCATAAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAGG  
 ATGGTTTTAAACACCTTTGTGAAATTGTCTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC  
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCATGCTTGGTTAGCATCTCCAACCTCC  
 TATGTAAATCAACAACCTGCATAATAATAAAAGGCAATCATGTTATA

**FIGURE 210**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLFLLTCELAEEVAAEEVEKSSDGFGAAQEPTWLTDVPAAMEFIAATEVAVIG  
FFQDLEIPAVPILHSMVQKFPGVSGISTDSEVLTHYNITGNTICLFRDVDNEQLNLEDEDI  
ESIDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAA  
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVQHVQNF  
CDGFLSGKLLKENRESEGKTPKVEL

**Signal peptide:**

amino acids 1-20

**Transmembrane domain:**

amino acids 143-162

**FIGURE 211**

GGAGAGCCGCGGCTGGGACCGGAGTGGGGAGCGCGGCGTGGAGGTGCCACCCGCGCGGGTG  
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACTCAGCGGGGACCCGGGCTCAGG  
 GACGCGGCGGCGGCGGCGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGAGCCGGG  
 GCGGTGATTGCAGCCCCAGACAGCCGGCGCTGGCTGTGGTGGTGTGCGGTGCTGGCGGCGCGCTTGG  
 GCTCTTGACAGCTGGAGTATCAGCCTTGGAGTATATACGCCAAAAGAAATCTTCGTGGCAA  
 ATGGTACACAAGGGAAGCTGACCTGCAAGTTCAGTCTACTAGTACGACTGGCGGGTTGACC  
 TCAGTCTCCTGGAGCTTCCAGCCAGAGGGGGCCGACACTACTGTGTCTGTTTTTCCACTACTC  
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAATCAGCTGGGCTGGAG  
 ACCTTGACAAGAAAGATGCATCAATCAACATAGAAAATATGCAGTTTATACACAATGGCACC  
 TATATCTGTGATGTCAAAAACCTCCTGACATCGTTGTCAGCCTGGACACATTAGGCTCTA  
 TGTCTAGAAAAAGAAATTTGCCTGTGTTTTCCAGTTTGGGTAGTGGTGGGCATAGTTACTG  
 CTGTGGTCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTATAGAAGGAAA  
 AACTCTAAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTTGTACCAGTTAAGCAGGC  
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAGAGTCTGCCTTCTGGATCTCACC  
 AGGGCCAGTCATATATGCACAGTTAGACCACTCCGCGGACATCACAGTGACAAGATTAAC  
 AAGTCAGAGTCTGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAATACCTAGAACATATC  
 CTCAGCAAGAAACAAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCATTACCACATGT  
 AGCCTTGGAGACCCAGGCAAGGACAAGTACACGTGTACTCACAGAGGGAGAGAAAGATGTGT  
 ACAAAGGATATGTATAAATATTCTATTTAGTCATCCTGATATGAGGAGCCAGTGTGTCATGA  
 TGAAAAGATGGTATGATTCTAÇATATGTACCCATTGTCTGTGTTTTTGTACTTTCTTTTC  
 AGGTCATTTACAATTGGGAGATTTCAGAAACATTCCTTTCACCATCATTTAGAAATGGTTTG  
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTTCCAGTAGACATGGCCTTTTAATGTAAG  
 GGCTTAAGACTGATTAGTCTTAGCATTTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA  
 GCATACCCAGGCTGGCCTTTAGCACAGTATCAGTACCATTATTTTGTCTGCCGCTTTTAAAA  
 AATACCCATTGGCTATGCCACTTGAAAACAATTTGAGAAGTTTTTTTGAAGTTTTTCTCACT  
 AAAATATGGGGCAATTGTTAGCCTTACATGTTGTGTAGACTTACTTTAAGTTTGCACCCTTG  
 AAATGTGTCATATCAATTTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG  
 GTCACCTTCATTCTGGACAGTGTGGATCAATACGTGATTAGTAGAAAAATCCAAGCTTTTGCTT  
 GAGAACTTTTGTAACTGGAGAGTAAAAAGTATCGGTTTTTA

**FIGURE 212**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSVSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDDKDDASINIEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVWVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTCSTSESLSPVKQAPRKSPSDTEGLVKSLPSGSHQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

**Signal peptide:**

amino acids 1-37

**Transmembrane domain:**

amino acids 161-183

**FIGURE 213**

GCCGGCTGTGCAGAGACGCCATGTACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC  
 CCCGGGGGCTTGGCCTCAAGCTGCGGACGACGCGGGGTCCATCAGCGCGCGGGCTGCCGCC  
 TCTCGGCCACGGCTGGGTGCGGGGCTCGGGCTGGGGCTGGGGCTGCGGCTCGGGGTGAAGC  
 TGGCAGGTGGGCTGAGGGGCGGGCCCCGGCGCAGTCCCCCGGCGCCCCGACCTGAGGCG  
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTCGCCCCGTGGTCTCCGACAGCCCCGCG  
 GCCGCCCTGCTCCAGGTGCTTCGCCAGAGCCATCGAGAGCAGCCGCGACCTGCTGCACAGGA  
 TCAAGGATGAGGTGGGCGCACCGGGCATAGTGGTTGGAGTTTCTGTAGATGGAAAAGAAGTC  
 TGGTCAGAAGGTTTAGGTTATGCTGATGTTGAGAACCGGTGACCATGTAAACCAGAGACAGT  
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTTGCTCTTGCCAAATTGTGGGAAG  
 CAGGGAACTGGATCTTGATATTCCAGTACAACATTATGTTCCCGAATTCCCAGAAAAAGAA  
 TATGAAGGTGAAAAGGTTTCTGTCAACAAGATTACTGATTTCCCATTTAAGTGAATTTCG  
 TCATTATGAAAAGGACATAAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTTGAAGATGA  
 TGAAAGAGAATGTTGCATTTGAGCAAGAAAAAGAAGGCAAAAGTAATGAAAAGAATGATTTT  
 ACTAAATTTAAAAACAGAGCAGGAGAATGAAGCCAAATGCCGAATTCAAAACCTGGCAAGAA  
 AAAGAATGATTTTGAACAAGGCGAATTATATTGAGAGAAAAGTTTGAAAATTC AATTGAAT  
 CCCTAAGATTATTTAAAAATGATCCTTTGTTCTTCAAACCTGGTAGTCAGTTTTTGTATTCA  
 ACTTTTGCTATACCTACTGGCAGCCATAGTAGAGAGAGCTTCAGGATGTAAATATTTGGA  
 CTATATGCAGAAAATATTCCATGACTTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC  
 CAGTGATTTACAATAGAGCAAGGTAAATGAATACCTTCTGCTGTGCTAGCTATATCGCATC  
 TTAACACTATTTTATTAATTTAAAAGTCAAATTTCTTTGTTTCCATTCCAAAATCAACCTGC  
 CACATTTTGGGAGCTTTTCTACATGCTGTTTTCTCATCTGTAAAGTGAAGGAAGTAAACA  
 TGTTTATAAGTAAAAAAA



**FIGURE 214**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQRAGLPPLGHGWVGGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQESLAPWSPQTPAPPCSRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVCKPETVMRIASISKSLTMVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLAAIVERASGCKYLDYMQKIFHDLMLTTVQEENEPVIYNRAR
```

**Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 39-60

**FIGURE 215**

GTGACACTATAGAAGAGCTATGACGTCGCATGCACGCGTACGTAAGCTCGGAATTCGGCTCG  
 AGGCTGGTGGGAAGAAGCCGAG**ATG**GCGGCAGCCAGCGCTGGGGCAACCCGGCTGCTCCTGC  
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGCCCCGGGCAGCGGCTGCCGGGCCGGGACT  
 GGTGCGCGAGGGGCTGGGGCGGAAGGTCGAGAGGGCGAGGCCTGTGGCACGGTGGGGCTGCT  
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACTTCCGGAAGCGGGGCTCACTGCTCT  
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGGCAGCTCAGCGAGGAGGAGCGGGGC  
 CGACTCCGGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCCGATCCCAAGGCGACCCGG  
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTTGTCCCTGCGTGCTCCCTGG  
 TGGAGTCGCACCTGTCGGACCAGCTGACCCTGCACGTGGATGTGGCCGGCAACGTGGTGGGC  
 GTGTGGTGGTGACGCACCCCGGGGGCTGCCGGGGCCATGAGGTGGAGGACGTGGACCTGGA  
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACCACAGCCCCAGGCCCTGAGACGGCGG  
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCCAGAAGGCCAAGAACCCCAAGGAGCAGAAG  
 TCCTTCTTCGCCAAATACTGGATGTACATCATTCCTCGTCTGTTCTCATGATGTCAGG  
 AGCGCCAGACACCGGGGGCCAGGGTGGGGGTGGGGGTGGGGGTGGTGGTGGGGGTAGTGGCC  
 TTTGCTGTGTGCCACCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACATTGAAATGTG  
 TGAACGTTTTTGAAGAGCTACAGCTTCCAGCAGCCAAAAGCAACTGTTGTTTTGGCAAGACGG  
 TCCTGATGTACAAGCTTGATTGAAATTCAGTGCTCACTTGATACGTTATTAGAAAACCAAG  
 GAATGGCTGTCCCATCCTCATGTGGCTGTGTGGAGCTCAGCTGTGTTGTGTGGCAGTTTAT  
 TAAACTGTCCCCAGATCGACACGCAAAAAAAAA

**FIGURE 216**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCRAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLLWNQQDGTLSLSQRQLSEEERGLRDVAALNGLYRVRIPRRFGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEQKSFFAKYWYIIPVVLFLMMSGAPDTGGQ
GGGGGGGGGGSGLCCVPPSL
```

**Signal peptide:**

amino acids 1-24

**Transmembrane domain:**

amino acids 226-243

**FIGURE 217**

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGGAGCCACAGCGGGGAGGGTGGCCTGGCGGCCT  
 GGAGCCGGACGTGTCCGGGGCGTCCCGCAGACCGGGGCAGCAGGTGCTCCGGGGGCCACC  
**ATG**CTGGTGACTGCCTACCTTGCTTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAAC  
 GTCAAGATGCCGGGCTAAACCCCTGGAAGGCCTGCAGCAATCCCTCCTTCCGTTTC  
 AACTGGACTTCTATCAGTCTACTTCTTGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC  
 CTCTATAAAGCTTACCAGCATTACTACTTCTGGAAGGTCAAATGCCATCCTCTATGCTG  
 TGGCCTTGCCCTCTACAGTCTCTTTGGCCTAGTGGCCTCCTCCCTTGTGGATTGGCTGGGTC  
 GCAAGAATCTTTGTGCTCTTCTCCCTGACTTACTCACTATGCTGCTTAACCAAACCTCTCT  
 CAAGACTACTTTGTGCTGCTAGTGGGGCGAGCACTTGGTGGGCTGTCCACAGCCCTGCTCTT  
 CTCAGCCTTCGAGGCCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT  
 GGATCCCAGCTACCTTTGCTCGAGCTGCCCTTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT  
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGGCCTGTAGCGCCCTTGTGGCTGC  
 CATCCCTCTCCTGGCTCTGGCAGGGGCCCTTGGCCCTTCGAAACTGGGGGGAGAACTATGACC  
 GGCAGCGTGCCCTTCTCAAGGACCTGTGCTGGAGGCCCTGCGCTGCCTCCTGTGCGACCGCCGC  
 GTGCTGCTGCTGGGCACCATAACAAGCTCTATTTGAGAGTGTGCTTCTCATCTTTGTCTTCT  
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGGCATTATCTTCTCCAGCTTCATGG  
 CAGCCAGCCTGCTTGGCTCTTCCCTGTACCGTATCGCCACCTCCAAGAGGTACCACCTTCAG  
 CCCATGCACCTGCTGTCCCTTGTGCTGCTCATCGTGTCTTCTCTCTTCTCATGTTGACTTT  
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCCTTCATAGCCTTTCTACTTATTGAGT  
 TGGCTTGTGGATTATACTTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA  
 GAGCAGGCTGGTGTACTCAACTGGTCCGGGTACCTTGCACCTACTGGCTTGCCATGGGCT  
 CCTTGCTCCCATGACAGTGATCGAAAAACAGGCACTCGGAATATGTTACAGCATTTGCTCTG  
 CTGTCATGGTGATGGCTCTGCTGGCAGTGGTGGGACTCTTACCGTGGTAAGGCATGATGCT  
 GAGCTGCGGGTACCTTACCTACTGAGGAGCCCTATGCCCTGAGCTG**TAA**CCCCACTCCAG  
 GACAAGATAGCTGGGACAGACTCTTGAATTCAGCTATCCGGGATTGTACAGATCTCTCTGT  
 GACTGACTTTTGTGACTGTCTGTGGTTTCTCTGCCATTGCTTTGTGTTTGGGAGGACATGA  
 TGGGGGTGATGGACTGGAAGAAGGTGCCAAAGTCCCTCTGTGTTACTCCCATTTAGAAA  
 ATAACACACTTTTAAATGATCAAAAAAAAAA

**FIGURE 218**

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPY  
 LYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTYSLCCLTKLS  
 QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHVLAVVAG  
 VAAEAVASWIGLGPVAPFVAIPLALAGALALRNWGENYDRQRAFSTRCAGGLRCLSDRR  
 VLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAASLLGSSLYRIATSKRYHLQ  
 PMHLLSLAVLIVVFSLEMLTFSTSPGQESPVESFIAFLLELACGLYFSPMSFLRRKVI PET  
 EQAGVLNWFRVPLHSLACLGLVLHDSDRKTGTRNMFISCSAVMMALLAVVGLFTTVVRHDA  
 ELRVPSPTTEEPYAPEL

**Signal peptide:**

amino acids 1-18

**Transmembrane domain:**

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,  
 314-330, 343-359, 379-394, 410-430

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**FIGURE 219**

GCGACGCGCGCGGGGCGGCGAGAGGAAACGCGGCGCCGGGCGGGCCCGGCCCTGGAG**ATG**  
 GTCCCCGGCGCGCGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGCCCA  
 CGGCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACA  
 TCTTCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATT  
 CACCTTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACCTCAGAACGGTTTCTTCATCCA  
 GGACCAGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCTCTCCAAGACTCGGGTGGTCC  
 AGGAGCACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTAC  
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCTGCTCGG  
 CCGAGACGGCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTT  
 CCATCCCAGTCAATGTACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTC  
 TGG**TAGA**AGAGTTTGTCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC  
 AGGAATTTTGCTACTTGGAAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGA  
 AAAGGGTTTGGGCGTTGCTAGGCTGAAAGGGAAGCCACCACTGGCCTTCCCTTCCCCAGG  
 GCCCCAAGGGTGCTCATGTCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTA  
 GAACCCGAAACAAAAGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACT  
 CACCTGGCTCCAGCTCCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGG  
 AGTGGTTTAAAGAGCTGGTGTGTTGGGGACTCAATAAACCCCTCACTGACTTTTTAGCAATAAA  
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 220**

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNQFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIIISDNAVNDNSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

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**Signal peptide:**

amino acids 1-20

**FIGURE 221**

TCTGCCTCCACTGCTCTGTGCTGGGATCATGGAACTGCACTGCTGTGTGGGCTGGTGGTGA  
 TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG  
 ACTGGGAAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGCACTGCGGACTAGGTGGCAG  
 AGGCCAACCCAAAGATGCCACGGACTGGTGTGCTGCCAGACCCATGACTGCTGCTATGACCACC  
 TGAAGACCCAGGGGTGCGGCATCTACAAGGACAACAACAAAGCAGCATACATGTATGGAT  
 TTATCTCAACGCTATTGTTTAATGGCTGTGTTAATGTGATCTATCTGGAAAATGAGGACTC  
 CGAA**TAAAA**AGCTATTACTAWTTNAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA  
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**FIGURE 222**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCgiYKDNNKSSIHCMdLSQRYCLMAVFNVIYLENEdSE
```

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 1-24

**N-glycosylation site.**

amino acids 86-89

**N-myristoylation sites.**

amino acids 20-25, 45-50

**Phospholipase A2 histidine active site.**

amino acids 63-70

**FIGURE 223**

CTCGCTTCTTCTTCTGGATGGGGGCCAGGGGGGCCAGGAGAGTATAAAGGCGATGTGGAG  
GGTGCCCGGCACAACCAGACGCCAGTCAAGGCGAGAGCCCTGGGATGCACCGGCCAGAGG  
CCATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTAT  
GGCCCTGGAGGAGGCAAGTATTTTCAGCACCACTGAAGACTACGACCATGAAATCACAGGGCT  
GCGGGTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCAGGTGAAACTTGGAGACTCCTGGG  
ACGTGAAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCAACCTGCAGCCAGGCGAATAC  
ATCACAAAAGTCTTTGTGCGCTTCCAAGCTTTCTCCGGGGTATGGTCATGTACACCAGCAA  
GGACCGCTATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG  
AGGGGCAGGTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGC  
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC  
AGCAAACCTACCCGTGGGTCGCTTAGGGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGT  
GTGGTGGTGGCTGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATA  
AATAAAGCTTCTGCAGAAAA

**FIGURE 224**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVK
LGDSWDVKLGALGNTQEVTLQPGYITKVVFVAFQAFLRGMVMYTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGYQLLGIKISIGFEWNYPLEEPTTEPPVNLTYSANSPVGR
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**Signal peptide:**

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**FIGURE 225**

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTTCTGGGCTCCAACGCAGCTCTGTGGCT  
 GAAGTGGGTGCTCATCAGGGAACTGCTGGGCTATGGAATACAGATGTGGCAGCTCAGGTAG  
 CCCCAAATTGCTTGAAGAAATACATCATGTTTTTCGATAAGAGAAATGTAGGATCCAGTT  
 TTTTTTTTAAACGCCCCCTCCCCACCCCCAAAAAACTGTAAAGATGCAAAAACGTAATAT  
 CCATGAAGATCCTATTACCTAGGAAGATTTTGATGTTTTGCTGCGAATGCGGTGTTGGGATT  
 TATTTGTCTTGGAGTGTCTGCGTGGCTGGCAAAGAATAATGTTCCAAAATCGGTCCATCT  
 CCCAAGGGGTCCAATTTTTCTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG  
 ACAGGGGCTGTCATGCAACTGGCCCTAAGCCAAAGCAAAAGACCTAAGGACGACCTTTTGAA  
 CAATACAAAGGATGGGTTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT  
 ATAGCCCCACTGTCTTACTGACAATGCTTCTCTGCGCAACGAGGATGCCCTAAGGGCTG  
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAAATTACAGGAGATACCCTCAAGTA  
 TATCTGCTGGTTGCTTAGGTTTGTCCCTTCGTATAACAGCCTTCAAAAACCTTAAGTATAAT  
 CAATTTAAAGGGCTCAACCAGCTCACCTGGCTATACCTTGACCATAACCATATCAGCAATAT  
 TGACGAAAATGCTTTTAATGGAAATACGCAGACTCAAAGAGCTGATTCTTAGTTCCAATAGAA  
 TCTCCTATTTTCTTAACAATACCTTCAGACCTGTGACAAATTTACGGAACCTTGGATCTGTCC  
 TATAATCAGCTGCATTCTCTGGGATCTGAACAGTTTCGGGGCTTGCGGAAGCTGCTGAGTTT  
 ACATTTACGGTCTAACTCCCCTGAGAACCATCCCTGTGCGAATATTCCAAGACTGCCGCAACC  
 TGGAACTTTTGGACCTGGGATATAACCGGATCCGAAGTTTAGCCAGGAATGTCTTTGCTGGC  
 ATGATCAGACTCAAAGAACCTCACCTGGAGCAATCAATTTTCCAAGCTCAACCTGGCCCT  
 TTTTCCAAGGTTGGTCAGCCTTCAGAACCTTTACTTGCAGTGGAAATAAAATCAGTGTCTATAG  
 GACAGACCATGTCTTGGACCTGGAGCTCCTTACAAGGCTTGATTATCAGGCAATGAGATC  
 GAAGCTTTTCAGTGGACCCAGTGTTCCTCAGTGTGTCGGAATCTGCAGCGCTTCAACCTGGA  
 TTCCAACAAGCTCACATTTATGGTCAAGAGATTTTGGATTCTTGGATATCCCTCAATGACA  
 TCAGTCTTGTGGGAATATATGGGAATGCAGCAGAAATATTGCTCCCTGTAACTGGCTG  
 AAAAGTTTTAAAGTCTAAGGGAGAATACAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG  
 AGTAAATGTGATCGATGCAGTGAAGAACTACAGCATCTGTGGCAAAGTACTACAGAGAGGT  
 TTGATCTGGCCAGGGCTCTCCCAAAGCCGACGTTTAAGCCCAAGCTCCCCAGGCCGAAGCAT  
 GAGAGCAAACCCCTTTGCCCCGACGGTGGGAGCCACAGAGCCCGGCCAGAGACCGATGC  
 TGACGCCGAGCACATCTCTTTCCATAAAATCATCGCGGCGAGCGTGGCGCTTTTCTGTCCG  
 TGCTCGTCACTCTGTGTTATCTACGTGTGTCATGGAAGCGGTACCTCGCAGCATGAAGCAG  
 CTGCAGCAGCGCTCCCTCATGCGAAGGCACAGGAAAAAGAAAAGACAGTCCCTAAAGCAAT  
 GACTCCCAGCACCGGAATTTTATGTAGATTATAAACCCCAACACAGGAGACCGGAGA  
 TGCTGCTGAATGGGACGGGACCTGCACCTATAACAAATCGGGCTCCAGGGAGTGTGAGGTA  
**TGA**ACCATTGTGATAAAAAGAGCTCTTAAAGCTGGGAAATAAAGTGGTCTTTATTGAACCT  
 TGGTGACTATAAGGGAACGCATGCCCCCTCCCTTCCCTCTCCTCTCACTTTGGTGG  
 CAAGATCCTTCTTGTCCGTTTTAGTGCATTATAATACTGGTCATTTCTCTCATACATA  
 ATCAACCCATTGAAATTTAAATACCACAATCAATGTGAAGCTTGAACCTCCGGTTAATATA  
 TACCTATTGTATAAGACCTTTACTGATTCCATTAAATGTGCGATTGTTTTAAGATAAACT  
 TCTTTCATAGGTAAAAAAAAAA

**FIGURE 226**

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFNVIRLLSGSAVALVIAPTPLLTLSSAERGCPCGRCCEGKMVYCESQKLQEIPSSISAG
CLGLSLRYNSLQKLKYNQFKGLNQLTWLYLDHNNHISNIDENAFNGIRRLKELISSNRISYF
LNNTFRPVTNLRNLDLNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRIQDCRNLELL
DLGYNRIRSLARNVVFAGMIRLKLHLEHNQFSKLNALFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRLDLGSGNEIEAFSGSPVFCVFNLRNLDSNKLTFIGQEILDSWISLNDISLA
GNIWECSRNICSLVNWLSFKGLRENTIICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPLPPTVGATEPGPETDADAEHISFHKKIAGSVALFLSVLVI
LLVIYVSWKRYPASMQLQQRSLMRRHRKKRQSLKQMTPTSTQEFYVDYKPTNTTETSEMLLN
GTGPCTYNKSGSRECEV
```

**Important features of the protein:****Signal peptide:**

amino acids 1-33

**Transmembrane domain:**

amino acids 420-442

**N-glycosylation sites.**

amino acids 126-129, 357-360, 496-499, 504-507

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 465-468

**Tyrosine kinase phosphorylation site.**

amino acids 136-142

**N-myristoylation sites.**

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

**FIGURE 227**

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAAACCACTATCCTAAGTTGACTGTCCTT  
TAAAT**ATG**CTCAAGATCCAGACTTTTCAGTGTCACCTCAGCGATCTCAACGATAGGGATCTTG  
TGTTTGCCGCTATTCCAGTTGGTGCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGTGT  
AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTTGG  
TGGCAGCTCTTCTCTGTGGAGCTGTGGTCCCTCGCCTCCAGTGCTGGGTGAGGAGACCCCGA  
ATTGATTCTCACAGGCGACCATGGCAGTTTTTGTCTGTTGGAGACTTGGACTCTATTTATGG  
GACAGAAGCAGCTGTGAGTCCAACCTGTTGGAATTCACCTTCAAACCTCAAACCCCTGACCTAT  
ATCCTGTTCTGCTCCATGTTTTTGGCCCTTTAGGCTCCCCACCTCCATATGAAGAAATTGTA  
AAAACAAC**TGAT**TTTTAGGTGTGGATTATCAATTTAAAGTATTAACGACATCTGTAATTCCA  
AAACATCAAATTTAGGAATAGTTATTTAGTTGTTGGAAATGTCCAGAGATCTATTCATATA  
GTCTGAGGAAGGACAATTCGACAAAAGATGGATGTTGGAAAAAATTTGGTCATGGAGATG  
TTTAAATAGTAAAGTAGCAGGCTTTTGATGTGTCACTGCTGTATCATACTTTTATGCTACAC  
AACCAAATTAATGCTTCTCCACTAGTATCCAACAGGCAACAATTAGGTGCTGGAAGTAGTT  
TCCATCACATTTAGGACTCCACTGCAGTATACAGCACACCATTTTCTGCTTTAAACTCTTTC  
CTAGCATGGGGTCCATAAAAAATTATTATAATTTAACAATAGCCCAAGCCGAGAATCCAACAT  
GTCCAGAACCAGAACCAGAAAGATAGTATTTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA  
GAAAAGTTTGGAGTTGAAGGGTAAAGGATAAATGAAGAGGAAAAGGAAAAGATTACAAGTCT  
CAGCAAAAACAAGAGGTTTTATGCCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA  
AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGGAGAAAAGAAAATTTCCC  
CTTTTACAGTAATGAATGTGGCTCCATAGTCCATAGTGTCTCTGGAGCCTCAGGCTTG  
GCATTTATTGCAGCATCATGCTAAGAACCTTCGGCATAGGTATCTGTTCCCATGAGGACTGC  
AGAAGTAGCAATGAGACATCTCAAGTGGCATTTTGGCAGTGGCCATCAGCAGGGGGACAGA  
CAAAAACATCCATCACAGATGACATATGATCTTCAGCTGACAAATTTGTTGAACAAAAACAAT  
AAACATCAATAGATATCTAAAAA

**FIGURE 228**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSIAISTIGILCLPLFQLVLSDLPCCEEDMCVNYNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPTVGIIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

**Signal peptide:**

amino acids 1-29

**Transmembrane domain:**

amino acids 52-70

**FIGURE 229**

GAGCGGAGTAAAACTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACCGGCGT  
 TTCTCCAGCTCGATCTGGAGGCTGCTTCGCCAGTGTGGGAGCGAGCTGACGCCCGCTTATTA  
 GCTCTCGCTGCGCTCGCCCGGCTCAGAAAGCTCCGTGGCGGGCGGACCGGTGACGAGAGGCC  
 ACGGCCAGCTCAGTTCCTCTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTTAAACT  
 CCCTCTTCAAACTCATCTCTGGGTGACTGAGTTAATAGAGTGGATACAACTTGCTGAAG  
 ATGAAGAATATACAATATTGAGGATATTTTTTCTTTTTTTTTTCAAGCTTGTGATTGTGGC  
 TTACCTCAAGTTACCATTTCCTCAGTCAAGTCTGTTTGTGCTTCTCAGAAATGTTTTTTA  
 CAATCTCAAGAAAAAATATGTCCAGAAATTGAGTTTACTGTGTGCTTGTATTGAGACTCAIT  
 TGGGGATTGATGTTACTGCACATATACTTTCAACAACCAAGACATCAAAGCAGTGTCAAGTT  
 ACGTGAGCAAACTACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAAATAAGA  
 ACACAGTGGATGTCGAGAACGGTGCTTCTATGGCAGGATATGCGGATCTGAAAAGAACAATT  
 GCTGTCTTCTGGATGACATTTTGCAACGATTGGTGAAGCTGGAGAACAAGTTGACTATAT  
 TGTGTGAATGGCTCAGCAGCCAAACCCCAATGGTACTAGTGGGAATTGTGTGCCAGTAA  
 CCACAAATAAAAAGAACGAATGTCCTCGGCCAGTATCAGATAGCAGTTGAAAATCACCTTGTGC  
 TGCTCCATCCACTGTGGATTATATCCTATGGCAGAAAAGCTTTATAATTGCTGGCTTAGGAC  
 AGAGCAATACTTTACAATAAAAGCTCTACACATTTTCAAGGAGTATGCTGGATTTCATGGAAC  
 TCTAATTCGTACATATAAAAAATTTTAAAGTTATTTGTTGCTTTCAGGCCAAGTCTGTTCATG  
 CTGTACTATGTCCCTAAAGAGAATTTGGTAACTTGGTTGATGTGGTAAGCAGATAGGTGAGT  
 TTTGTATAAATCTTTTGTGTTGAGATCAAGCTGAAATGAAAACATGAAAACATGGATTTC  
 ATTTCTATAACACATTTATTTAAGTATATAACACGTTTTTTTGGACAAGTGAAGAATGTTTAA  
 TCATTCTGTCAATTTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTTGAAAAAATGTG  
 CTTATTGTACTATATTTTGTATTCCAATTATGAGCAGAGAAAGGAAATATAATGTTGAAAA  
 TAATGTTTTGAATCATGACCCAAAGAATGTATTGATTTGCACTATCCTTCAGAATAACTGA  
 AGGTTAATATTGTATATTTTTAAAAATTACACTATAAGAGTATAATCTTGAATGGGTAG  
 CAGCCACTGTCCATTACCTATCGTAAACATTGGGGCAATTTAATAACAGCATTAATAATAGTT  
 GTAACTCTAATCTTATACTTATGAAAGATAAAAGATATTTTATGATGAGAGTAAACAATA  
 AAGTATTCATGATTTTTCACATACATGAATGTTCAATTTAAAGTTTAACTCTTTGAGTGTCT  
 ATGCTATCAGGAAGCACATTTATTTCCATATTTGGGTAAATTTTGCTTTTATTATATTGGTC  
 TAGGAGGAAGGGACTTTGGAGAAATGGAACCTTGGAGACTTTAGCCAGGTGTATATAATAAA  
 GGTACTTTTTGTGCTGCATTAATTTGCTTGGAAAGTGTTAAACATTATATTATATAAGAGTATC  
 CTTTATGAAATTTTGAATTTGTATAACAGATGCATTAGATATTCATTTTATATAATGGCCAC  
 TTAATAATAAGACATTTAAAAATAAACTATGAAGATTGACTATCTTTTCAGGAAAAAGCT  
 GTATATAGCACAGGGAACCCCTAATCTGGGTAACTTAGTATAAAACAAATTACTTTTTAT  
 TTAATTTTCCCTTTAGCAAACTCAATTGCCACATGGTGCCCTATATTTTCATAGTATTATAT  
 CTCTATAGTAACCTGCTTAAGTGCAGCTAGCTTCTAGATTTAGACTATATAGAATTTAGATAT  
 TGTATTGTTTCGTCATTATAATATGCTACCACATGTAGCAATAATTAACAATATTTTATTAATA  
 TAAATATGTGAAATATTGTTTCATGAAAGACAGATTTCCAATCTCTCTCTCTCTCTGTA  
 CTGCTACCTTTATGTGAAGAAATTAATTATATGCCATTGCCAGGT



**FIGURE 230**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMLLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTNKRRTNVSGSIR
```

**Important features of the protein:****Signal peptide:**

amino acids 1-26

**FIGURE 231**

CGCGGCCGGGCCCGGGGGTGAAGCTGCCAGGCGGGCTGTGGCGCAGGCTTCCAGCCCCAC  
**CATG**CCGTGGCCCTGCTGCTGCTGCTGGCCGTGAGTGGGGCCCCAGACAAACCGGCCATGCT  
 TCCCCGGGTGCCAATGCGAGGTGGAGACCTTCGGCCTTTTCAGACAGCTTCAGCCTGACTCGG  
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGTGCCATCCCTCTGGACACAGCCCA  
 CTTGGACCTGTCTCCAAACCGGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGGCCGGGCT  
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACTGCTCACCAGCATCTACCCACTGCC  
 TTCTCCCGCCTTCGCTAGCTGGAGTCGCTTGACCTCAGCCACAATGGCCTGACAGCCCTGCC  
 AGCCGAGAGCTTCACAGCTCACCCTGAGCGACGTGAACCTTAGCCACAACAGCTCCGGG  
 AGGTCTCAGTGTCTGCCTTCACGACGCACAGTCAGGGCCGGGCATACACGTGGACCTCTCC  
 CACAACCTCATTCACCGCCTCGTGCCCCACCCACGAGGGCCGGCCTGCCTGCCGCCACCAT  
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCGGTGCCAACCTCCGAGACTTGCCCC  
 TGCCTACCTGAGCCTGGATGGGAACCTCTAGCTGTCAATTGGTCCGGGTGCCTTCGCGGGG  
 CTGGGAGGCCTTACACACCTGTCTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG  
 TGGCTTCGGTGAAGTACCGGGCTGCAGGTCTCGGACCTGCGGGCAACCCCAAGCTTAAT  
 GGGCAGGAGCTGAGGTGTTTTAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTTCGGGCACC  
 AACCTGGTGCCCCCTGCCTGAGGCGCTGCTCCTCCACCTCCCGGCACTGCAGAGCGTCAGCGT  
 GGGCCAGGATGTGCGGTGCCGGCGCCTGGTCCGGGAGGGGCATCCGCCGGAGGCCCTGGCT  
 CCAGCCCCAAGGTGCCCTGCACTGCGTAGACACCCGGGAATCTGCTGCCAGGGGCCCAACC  
 ATCTCT**TGA**CAATGGTGTGGCCCCAGGGCCACATAACAGACTGCTGTCTGGGCTGCCTCAG  
 GTCCCCAGTAACCTATGTTCATGTGCCAACACAGTGGGGAGCCCGCAGGCCCTATGTGGCA  
 GCGTCAACCACAGGAGTTGTGGCCTAGGAGAGGCTTTGGACCTGGGAGCCACACCTAGGAGC  
 AAAGTCTCACCCCTTTGTCTACGTTGCTTCCCCAAACCATGAGCAGAGGGACTTCGATGCCA  
 AACCAGACTCGGGTCCCCCTCCTGCTTCCCTTCCCCACTTATCCCCCAAGTGCCCTTCCCTCAT  
 GCCTGGGCGCGCTGACCCGCAATGGGCAGAGGTGGGTGGGACCCCTGCTGCAGGGCAGA  
 GTTCAGGTCCATGGGCTGAGTGTCCCTTTGGGCCCCATGGCCCCAGTCACTCAGGGGCGAGTT  
 TCTTTTCTAAACATAGCCCTTTCTTTGCCATGAGGCCATGAGGCCCGCTTCATCCTTTTCTAT  
 TTCCCTAGAACCTTAATGGTAGAAGGAATTGCAAGAATCAAGTCCACCTTCTCATGTGAC  
 AGATGGGAAACTGAGGCCTTGAGAAGGAAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC  
 ATGACTGGAGCACAGCCTTCCTGCCTCCAGCCCGGACCCCAATGCACTTTCTGTCTCCTCTA  
 ATAAGCCCCACCTTCCCGCCTGGGCTCCCTTGTGCTGCCCTGCTGTTCCCCATTAGCACA  
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAGTGGGACTCTGGGCCTCTGACAGCT  
 GTGGCGCATGGGCTAAGTCACCTGCGCCTTCGGAGCCTCTGGAAGCTTAGGGCAGCTTGGTT  
 CCAGCCTAGCCAGTTTCTCACCTCGGGTTGGGGTCCCCAGCATCCAGATCGGAAACCTACC  
 CATTTTCCCTGAGCATCTCTAGATGCTCCCCAAGGAGTTGTGCACTTCTGGAGCCTCA  
 TCTGGCTGGGATCTCCAAGGGCCTCCTGGATTGACCTCCCACTGGCCCTGAGCAGCAGCA  
 CCTTCTTACCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCCGACCCATGTCTATGC  
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCTGGGCTGTTTCTTAGTCTTCATTTTA  
 TAAAAGTTGTGCTTTTAAACGGAGTGCACTTTCAACGGCCCTCCCTACCCCTGCTGGC  
 CGGGGATGGAGACATGTCAATTGTAAAGCAGAAAAAGGTTGCATTTGTTCACCTTTTGTAA  
 ATTGTCCTGGGCTGTGTTGGGTTGTTGGGGGAAGCTGGCCATGAGTGGCCACATGGGCATC  
 AGGGGCTGGCCCCACAGAGACCCCAAGGCGAGTGAGCTGTGCTTCCCCACCTGCCTAGC  
 CCATCATCTATCTAACCGGTCTTGATTTAATAAACAGCTATAAAAGGTTTAAAAA  
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

**FIGURE 232**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVSAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDLPLRYLSLDGNPLAVIGPGAFAGLGGLTHLSLASLQRLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDSGTNLVPLPEALLLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

**Signal peptide:**

amino acids 1-16

**Transmembrane domains:**

amino acids 215-232, 287-304

**FIGURE 233**

GATGGCGCAGCCACAGCTTCTGTGAGATTCGATTTCTCCCGAGTTCCTGTGGGTCTGAGG  
 GGACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCA  
 AAACAAGTTTTGACATTTCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT  
 GTTCCAGGCCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGC  
 CACGACCTGTGCCACCACTCGCACTCAGACTCTGAAGTCAAGCTGAAATCTTCTCTTCAC  
 GGGAGGCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCC  
 TCTAGTCTTGCCCTTCAGCCTTCTCTCTGTGCGTTTTATCTCCTATGGACTCCTTCCACTGG  
 ACTGAAGACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATG  
 GATTTTCTGAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTA  
 AGGAGGACTGAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTT  
 GCTAAGACTCTATCTGGACAGGGTATTTAAAACTACCAGACCCTGACCATTATACTCTCC  
 GGAAGATCAGCAGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCAT  
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA  
 CTTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAAGTACAGATTCTTC  
 TGCAATGGATGGAGGAGACAGAAATAGGAGGAGAAAGTGATGCTGCTGCTAAGAATATTCGAGGT  
 CAAGAGCTCCAGTCTTCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTTACT  
 GTACTAGTCTTGTGCTGGTCAAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGAT  
 TGTCTTTATGCATCCCCAATCTTAATTGAGACCATACTGTATAAGATTTTTGTAATATCTT  
 TCTGCTATTGGATATATTTATTAGTTAATATATTTATTTATTTTGTCTATTTAATGTATTT  
 ATTTTTTTACTTGACATGAACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAG  
 AGCAGGTGATGTATTTTATACAGTAAAAAAGAACCTTGTAATTTAGAAAGAGTGGCT  
 AGGGGGGTATTTCATTTGTATCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGA  
 TATTTGAAATGAACCAATGACTACTTAGGATGGGTTGTGGAATAAGTTTTGATGTGGAATT  
 GCACATCTACCTTACAATTACTGACCATCCCCAGTAGACTCCCCAGTCCCATAAATTGTGTAT  
 CTTCCAGCCAGGAATCTACACGGCCAGCATGTATTTCTACAAATAAGTTTTCTTTGCATA  
 CCAAAAAAAAAAAAAAAAAA

**FIGURE 234**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500  
><subunit 1 of 1, 261 aa, 1 stop  
><MW: 29667, pI: 8.76, NX(S/T): 0  
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP  
EIFSSREAWQFFLLWLSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL  
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVFKNYQTP  
DHYTLRKISSLANSLFTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQAAVVKALG  
ELDILLQWMEETE

**Important features of the protein:****Signal peptide:**

amino acids 1-42

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 192-195, 225-228

**N-myristoylation sites.**

amino acids 42-47, 46-51, 136-141

**FIGURE 235**

CCGTTATCGTCTTGCGCTACTGCTGA**ATG**TCCGTCCCGGAGGAGGAGGAGAGGCTTTTGCCG  
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCCTACTGTCCGGCTGCGCGGCTACCGTGGC  
 CGAGCTAGCAACCTTTCCCTGGATCTCACAAAACTCGACTCCAATGCAAGGAGAAGCAG  
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCCACA  
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTTGGCAAGGAGTGACACCGCCAT  
 TTACAGACACGTAGTGTATTCTGGAGGTCGAATGGTCACATATGAACATCTCCGAGAGGTTG  
 TGTGTTGGCAAAAGTGAAGATGAGCATTATCCCCTTTGGAAATCAGTCATTGGAGGGATGATG  
 GCTGGTGTATTGGCCAGTTTTTAGCCAATCCAACAGCTAGTGAAGGTTCAGATGCAAAAT  
 GGAAGGAAAAAGGAACTGGAAGGAAAACCATTGCGATTTCGTGGTGTACATCATGCATTTG  
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGGCTTTGGGCAGGCTGGGTACCCAATATACAA  
 AGAGCAGCACTGGTGAATATGGGAGATTTAACCACTTATGATACAGTGAACACTACTTGGT  
 ATTGAATACACCACTTGAGGACAATATCATGACTCACGGTTTATCAAGTTTATGTTCTGGAC  
 TGGTAGCTTCTATTCTGGGAACACCAGCCGATGTATCAAAAGCAGAATAATGAATCAACCA  
 CGAGATAAACAAGGAAGGGGACTTTTGTATAAATCATCGACTGACTGCTTGATTAGGCTGT  
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTTACCATCTTGCTGAGAATGACCC  
 CTTGGTCAATGGTGTCTTGCTTACTTATGAAAAATCAGAGAGATGAGTGGAGTCAGTCCA  
 TTT**TAA**

**FIGURE 236**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIIEEGFLKLWQGVTPAIYRHVVYSGGRMVITYEHLREVVFVGKSEDEH
YPLWKSIVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVLNTPLEDNIMTHGLSSLCSGLVASILGTP
ADVIKSRIMNQPRDKQGRGLLYKSSTDCLIQAVQGEFMSLYKGFPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

**Transmembrane domains:**

amino acids 25-38, 130-147, 233-248

**FIGURE 237**

CGGACGCGTGGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCTCCTTCCTGCGCGCGC  
 GCCTGAAGTCGGCGTGGGCGTTTGAGGAAGCTGGGATACAGCATTTAATGAAAAATTTATGC  
 TTAAGAAGTAAAAATGCGCAGGCTTCTAGATAATTTTCGTTGCCAGAATGTGAATGTATTG  
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGTGCGAGGTATATTGTTTTTACAGGC  
 TGGTGGAATAATGATTGATGCAGCTGTGGTGTATCCTAAGCCAGAACAGTTGAACCATGCCTT  
 TCACACATGTGGTGTATTTCCACATTGGCTTCTTCATGATAAATGCTGTATCCAATGCTC  
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTTAGGAAGAACAGGTGCTCGAGTTTGGCTT  
 TTCATTGGTTTCATGTTGATGTTTGGGTCACTTATTGCTTCCATGTGGATCTTTTTGGTGC  
 ATATGTTACCCAAAATACTGATGTTTATCCGGGACTAGCTGTGTTTTTCAAATGCACTTA  
 TATTTTTTAGCACTCTGATCTACAAATTTGGAAGAACCGAAGAGCTATGGACCTGAGATCAC  
 TTCTTAAGTCACATTTTCCTTTTGTATATTCTGTTTGTAGATAGGTTTTTTATCTCTCAGT  
 ACACATTGCCAATGGAGTAGATTGTACATTAAATGTTTTGTTTCTTACATTTTTATGTTT  
 TGAGTTTTGAAATAGTTTTATGAAATTTCTTTATTTTCATTGCATAGACTGTTAATATGTA  
 TATAATACAAGACTATATGAATTGGATAATGAGTATCAGTTTTTTATTCTGAGATTTAGAA  
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTTGTCAATTTAGAAAGTAACCACTCTTGT  
 CTCTCTGGCTGGGCACGGTGGCTCATGCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGG  
 CCGATTGCTTGAGGTCAAGTGTTTGAGACCAGCCTGGCCAACATGGCGAAACCCATCTACT  
 AAAAAACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCAGCTACCTGGGAGGC  
 TGAGGCAGGAGAATCGCTTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTTGCGCCAC  
 TGCACCTCTAGCCTGGGGGAGAAAGTAACTCCCTCTCAAAAAAAGACCACTCTCAGTATC  
 TCTGATTTCTGAAGATGTACAAAAAATATAGCTTCATATATCTGGAATGAGCACTGAGCCA  
 TAAAAGTTTTTCAGCAAGTTGTAACCTATTTTGGCCTAAAAATGAGGTTTTTTTTGGTAAAGA  
 AAAAAATATTTGTTCTTATGTATTGAAGAAGTGACTTTTATATAATGATTTTTTAAATGCC  
 AAAGGACTAGTTTGAAGCTTCTTTTAAAAAGAATTCCTCTAATATGACTTTTATGTGAGAA



**FIGURE 238**

MAGFLDNFRWPECECIDWSERRNAVASVVAGILFFTGWWMIDAAVVYPKPEQLNHAFHTCG  
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ  
NTDVYPGLAVFFQNALIFFSTLIYKFGRTTELWT

**Important features:****Signal peptide:**

amino acids 1-44

**Transmembrane domains:**

amino acids 23-42 (type II), 60-80, 97-117, 128-148

**FIGURE 239**

GTTGATGGCAAACCTCCTCAAAGGAGGGGCAGAGCCTGCGCAGGGCAGGAGCAGCTGGCCCA  
 CTGGCGGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT  
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGGACTGTGAGAAGCTGGCCAGGGTGGT  
 GGTCAAGTGGGTGAGGACCTACGGCACCTGCTGGACCACCTCGCCTTCTCCATCGAAGCAG  
 GGAAGTGGGAGCCTCGAGCCTCGGGTGAAGCTGACCCCAAGCCACCCCTTACCTGGACAG  
**GATG**AGAGTGTGAGGTGTGCTTCGCCCTCCTGGCCCTCATCTTTGCCATAGTCACGACATGGA  
 TGTATTATTCGAAGCTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA  
 GCCTCGCCACCAAGGAGATCCAGGTTAAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC  
 AGCCAACTACTTTGCGTTTAAAAATCTGCAGTGGGGCCGCCAACGTCGTGGGCCCTACTATGT  
 GCTTTGAAGACCGCATGATCATGAGTCTGTGAAAAACAATGTGGGCAGAGGCCTAAACATC  
 GCCCTGGTGAATGGAACCAAGGAGCTGTGCTGGGACAGAAGGCATTTGACATGTACTCTGG  
 AGATGTTATGCACCTAGTGAAATTCCTTAAAGAAATTCGGGGGGTGCAGTGGTGTCTGGTGG  
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTTCTCTGACTTG  
 GGGAGTTCTACGCAAAACAACTGGGCTTCGGGGACAGCTGGGTCTTCATAGGAGCCAAAGA  
 CCTCAGGGGTAAAAGCCCTTTGAGCAGTTCTTAAAGAACAGCCAGACACAAACAAATACG  
 AGGGATGGCCAGAGCTGCTGGAGATGGAGGGCTGCATGCCCCGAAGCCATTT**TAG**GGTGGC  
 TGTGGCTCTTCTCAGCCAGGGGCCCTGAAGAAGCTCCTGCCTGACTTAGGAGTCAGAGCCCG  
 GCAGGGGTGAGGAGGAGGAGCAGGGGGTGTGCGTGGAAAGTGTGCAAGTCTTGCACGC  
 TGTGTGCGCCTCTCCTCGGAAACAGAACCTCCACAGCACATCTACCCGGAAGACC  
 AGCCTCAGAGGTCTTCTGGAACCAGCTGTCTGTGGAGAGAATGGGGTGTCTTTCGTGAGG  
 ACTGCTGACGGCTGGTCTGAGGAAGGACAACTGCCCAGACTTGAGCCCAATTAAATTTTA  
 TTTTGTGCTGTTTGAAAAAAAAAAAAAAAAAAAAA

**FIGURE 240**

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814  
<subunit 1 of 1, 224 aa, 1 stop  
<MW: 24963, pI: 9.64, NX(S/T): 1  
MRVSGVLRLLALIFAIVTTWMFIRSYSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP  
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVGRGLNIALVNGTTGAVLGQKAFDMYSG  
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKFLSDLGSSYAKQLGFRDSWVFIGAKD  
LRGKSPFEQFLKNSPD TNKYEGWPELLEMEGCMPPKPF

**Important features:****Signal peptide:**

amino acids 1-15

**ATP/GTP-binding site motif A (P-loop).**

amino acids 184-191

**N-glycosylation site.**

amino acids 107-110

**FIGURE 241**

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAGAGGCAGCAAGAGATTTGTCTGGGGAT  
 CCAGAAACCCATGATACCCCTACTGAACACCGAATCCCCTGGAAGCCCACAGAGACAGAGACA  
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTCTC  
 TCACTCCTCCCTCCCTCTCTCTCTGCCTGTCTAGTCTCTAGTCTCAAATCCCAGTCCC  
 CTGCAACCCCTTCTCTGGGACACTATGTTGTTCTCCGCCCTCTGCTGGAGGTGATTTGGATCC  
 TGGCTGCAGATGGGGGTCAACACTGGACGTATGAGGGCCACATGGTCAAGGACCATTGGCCA  
 GCCTCTTACCCTGAGTGTGGAACAATGCCAGTCGCCCATCGATATTAGACAGACAGTGT  
 GACATTTGACCCTGATTTGCCTGCTCTGCAGCCCCACGGATATGACAGCCTGGCACCAGAGC  
 CTTTGGACCTGCAACAATATGGCCACACAGTGCACCTCTCTCTGCCCTCTACCTGTATCTG  
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGGTCAGAAAGGATC  
 CCCAGGGGGGTGAGAACCAGATCAACAGTGAAGCCACATTTGCAGAGCTCCACATTGTAC  
 ATTATGACTCTGATTCCTATGACAGCTTGAGTGAGGTGCTGAGAGGCCCTCAGGGCCTGGCT  
 GTCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTTCTGAG  
 TCACTTGCAATGAAGTCAGGCATAAAGATCAGAAGACCTCAGTGCCCTCCCTTCAACCTAAGAG  
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACCTCCCCCT  
 TGCTACCAGAGTGTGCTCTGGACAGTTTTTTATAGAAGTCCCAGATTTCAATGGAACAGCT  
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAAGAGGAGCCCTCTAAGCTTCTGGTACAGA  
 ACTACCGAGCCCTTCAGCCTCTCAATCAGCGCATGGTCTTTGCTTCTTTTCATCCAAGCAGGA  
 TCCTCGTATACCACAGGTGAAATGCTGAGTCTAGGTGTAGGAATCTTGGTTGGCTGTCTCTG  
 CCTTCTCCTGGCTGTTTATTTCATTGCTAGAAAGATTCGGAAGAAGAGGCTGGAAAACCGAA  
 AGAGTGTGGTCTTCACTCAGCACAGCCACGACTGAGGCATAAATTCCTTCTCAGATACCA  
 TGGATGTGGATGACTTCCCTTCATGCCTATCAGGAAGCCTCTAAATGGGGTGTAGGATCTG  
 GCCAGAAACACTGTAGGAGTAGTAAGCAGATGTCTCCTTCCCCCTGGACATCTCTTAGAGAG  
 GAATGGAGCCAGGCTGTCAATCCAGGAAGAACTGCAGAGCCTTCAGCCTCTCCAAACATGTA  
 GGAGGAAATGAGGAAATCGCTGTGTTGTTAATGCAGAGANCAAACTCTGTTTAGTTGCAGGG  
 GAAGTTTGGGATATACCCCAAAGTCTCTACCCCTCACTTTTATGGCCCTTTCCCTAGATA  
 TACTCGCGGATCTCTCCTTAGGATAAAGAGTGTGCTGTTGAAGTTGTATATTTTGTATCAATA  
 TATTGGAAATTAAGTTTCTGACTTT

**FIGURE 242**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWFPASYPECGNNAQSPIDIQTDSVTFDPDLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKSGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTTPPCYQSVLWTVFYRRSQISMEQLEKLQGTI
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

**Important features of the protein:****Signal peptide:**

amino acids 1-15

**Transmembrane domain:**

amino acids 291-310

**N-glycosylation site.**

amino acids 213-216

**Eukaryotic-type carbonic anhydrases proteins**

amino acids 197-245, 104-140, 22-69

**FIGURE 243**

[illegible]

**FIGURE 244**

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSLSLIPLTQM  
LTLGPDLLHLLNPAAGMTFGTQTHPLTLGGLNVQQQLHPHVLPFVVTQLGAQGTILSSEE  
LPQIFTSLIIHSLFPGGILPITSQAGANPDVQDGSFPAGGAGVNPATQGTTPAGRLLTPSG  
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

**Signal peptide:**

amino acids 1-16

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**FIGURE 245**

GGAGAGAGGCGCGCGGGTGAAGGCGCATTGATGCAGCCTGCGGCGGCCCTCGGAGCGCGGCG  
 GAGCCAGACGCTGACCACGTTCCCTCTCCTCGGTCTCCTCCGCCCTCCAGCTCCGCGCTGCCCG  
 GCAGCCGGGAGCC**ATGC**GACCCCCAGGCCCGCCGCTCCCCGCAGCGGCTCCGCGGCCCTCC  
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCGCCGTCGAGCGCCTCTGAGATCCCCAAGGGGAAG  
 CAAAAGGCGCAGCTCCGGCAGAGGGAGGTGGTGGACCTGTATAATGGAATGTGCTTACAAGG  
 GCCAGCAGGAGTGCCCTGGTCGAGACGGAGCCCTGGGGCCAATGTTATCCGGGTACACCTG  
 GGATCCCAGGTCGGGATGGATTCAAAGGAGAAAAGGGGGAATGTCTGAGGGAAAAGCTTTGAG  
 GAGTCTGGACACCCAACTACAAGCAGTGTTTCATGGAGTTCATTGAATTATGGCATAGATCT  
 TGGGAAAATTGCGGAGTGATACATTTACAAAGATGCGTTCAAATAGTGCTCTAAGAGTTTTGT  
 TCAGTGGCTCACTTCGGCTAAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTTACATTC  
 AATGGAGCTGAATGTTTCAGGACCTCTTCCCATTGAAGCTATAATTTATTTGGACCAAGGAAG  
 CCTGAAATGAATCAACAATTAATATTCATCGCACTTCTTCTGTGGAAGGACTTTGTGAAG  
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTTGTTTCAGATTACCCAAA  
 GGAGATGCTTCTACTGGATGGAATTCAGTTTCTCGCATCATTATTGAAGAATACCAAAA**TA**  
**A**ATGCTTTAATTTTCATTTGCTACCTCTTTTTTTATTATGCCTTGGAATGGTTCACTTAAAT  
 GACATTTTAAATAAGTTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTTACAGA  
 CCAAAGTGTGATTTACACTGTTTTTAAATCTAGCATTATTCATTTTGCTTCAATCAAAGT  
 GGTTTCAATATTTTTTTTAGTTGGTTAGAATACTTTCTTCATAGTCACATTCTCTCAACCTA  
 TAATTTGGAATATTGTTGTGGTCTTTTGTCTTTTCTCTTAGTATAGCATTTTTTAAAAAATA  
 TAAAGCTACCAATCTTGTACAATTTGTAAATGTTAAGAATTTTTTTTATATCTGTTAAAT  
 AAAAATTATTTCCAACA



**FIGURE 246**

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGFAASPQRLRGLLLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLKIA
ECTFTKMRSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIEELPK
```

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 195-217